

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGACCTGGTGCACCCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCGGACACTACCTTCTAGGGTTTTCCACCCAGCTTTTACCACAGGCCCTCCCTGTTGTGAAGAATTCCATCACGAAGAATCAATGGCTGTTAACACCTAGCAGGGGAATATGCCACCAACAAAGAATTGGGATCCGGCGTGGGAAGACTGGCCAAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAATTTGATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTACTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGTATGTCAAGGATAGAATTCATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCTTTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTGGTGACAAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATACCATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGTGCAGTGGTGGCTCCTCTGACAAATATTAGGGGGTCCCTCTCTCATCAGAGCTGCATGGTACACAGCTGGCATTGTGGGAGGCCCTCCACTGTGGCCATGTGTGCCCCAGTGAAAAAGTTTCTGAACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATGTTTCTTCCACCTACCACCGTGGCTGGTGCACCTCTTTACTCAGTGGCAATGTACGGTGGATTAGTTCTTTTACAGCATGTTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAAGTATCACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTAATCTACATGGATACATTAATATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAAAGAAAT**AG**AGTGACTCAGCTTCTGGCTTCTCTGTACATCAAAATATCTTGTTTAAATGGGGCAGATATGCATTAATTAATTTGTACAAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCTATCATATTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGTAATCCTCTCCCAAATAAGCACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTTTGGTGAAATGTGAAAACTAAAGTTTGTGTGATGAGAATGTAAGTCTTTTTTCTACTTTAAAAATTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTTGATATTTTTTTGGAGTGCAGAAATGTGAATTTAATGTCTAATAAGTGATTTGGAGCTTTGGTAAAGGACAGAGAGAAGGAGTCACCTGCAGTCTTTTGTTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTAGTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAAACAAGTGGTCATTGTTACATTCAATTTGCTGAACTTAACAAAACCTGTTTCATCCTGAAACAGGCACAGTGATGCATTCTCCTGCTGTTGCTTCTCAGTGTCTCTTTCCAATATAGATGTGGTCATGTTGACTTGTACAGAATGTTAATCATACAGAGAATCCTTGATGGAATATATATGTGTGTTTTACTTTTGAATGTTTACAAAAGGAAATAAATTTAAACATTCTCAAGAGAAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAGATAACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFFVAGGAAVGLGALCYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTF AAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLS IYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCGCCGCTCTCCGCTTCTGCAT
CGCGGCTTCGGCGGCTTCACCTAGACACCTAACAGTCGCGGAGCCGCGCGCTCGTGAGGG
GCTCGGCACGGGAGTCGGCGGCTCTTGTGCATCTTGGCTACCTGTGGGTGCGAAGATGTCGG
ACATCGGAGACGTGGTTCAGGAGCATCCCGGCGATCAGCGCTATTGGTTCGCGCGCCACCGTC
GCGGTGCCCTTGGTCGGCAAACTCGGCCCTCATCAGCCGCGCCTACCTCTTCCCTCTGGCCGA
AGCCTTCCCTTTATCGCTTTCAGATTGGAGGCCAATCAGTCGCCACCTTTTATTTCCCTGTGG
GTCCAGGAAGTGATTCTTTATTGGTCAATTTATATTTCCTTATCAGTATCTACGGGA
CTTGAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTATTATCATGCTCCTCTTTAACTG
GATTTCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
TGTCACTACTTTATGCTCGGCCACGTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
ACACGATTTAAAGCCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
CTCGGTAATCAATGAGCTTATTTGGAATCTGGTTGGACATCTTTATTTTCTTAATGTTCA
GATACCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTGTGACCGCTGG
CTGCCAGTAGGAGAGGAGGAGTATCAGGATTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
TGCTGATCAGAATGGCGGAGGCCGAGACACAACCTGGGGCCAGGCTTTCGACTTGGAGACC
AGTCGAAGGGGCGGCCCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCCCACTGCTGGGTG
CACTTAACAACTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
AGTACGAGACAAGGTTTCTTAATCCGGAAGAAAAATATAAGTGTTCACAAGTTTCAAGAT
TCTCATTCAGTCCCTTACTGCTGTGAAGAACAATAACCACTGTGCAAAATGCAAAATGAC
TACATTTTGGTCTCTCTCTCTCCCTTTCCGTCTGAATAATGGTTTTCAGCGGTCTCT
AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAACCTTCCCAAAGGACCTTATCTCTT
CTTTGCACATAGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
CCCATAAATTTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGTC
ACAACAATCATATTACGTTATTTTCCCTTTTGGTGGCAGAATGTTACCAATAGGGGGAG
AAGACAGCCAGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCGTTGTT
AACCTTTTGCCACTTTCAGATATTTTATAAAAAAAGTACCCTGAGTTTCATGAGGGCCA
CAGATTGTTTATAATGACATACGAGGGTTGGTGCTGGGTGTTTGTCTCAGCTAAGTGA
TCAAGACTGTAGTGGAGTTGACGTAAACATGGGTAGGTTTAAACCATGGGGGATGCACCCC
TTTGCGTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTGCTTTGTGT
TAGGAGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTGTAGAGGTCCTGGGCATTG
ATTCCTATTTCAATCTCATTTGGAATATGTGTTCACTGAGTAAAGGAGGAGAGACCTCATA
CGCTATTTAAATGTCACTTTTGGCTATCCCCCGTTTGTGGTCAITGTTCAATTAATGT
GAGGAAGGCCGAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAAGGTGTGTTA
TTTTAGTCTGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTT
TCGTAGTGGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAAATAAGTTTGTGAAGGCCA
TGCTTTTTCACACAGTTATTTTATTATGACGTTATCTGAAAGCAGCTGTTAGGAGCAGT
ATTGAGTGGCTGTCACTTTTGGGCAACTAAAAAGGCTTCAAAAGCTTTTGTACGTTTCTT
TTCAGGAAGCATTTGCTTAAACAGTATGACTATCTTTCCCACTCTTAAACAGTGTGAT
GTGTGTTTATCTAGGAAATGAGAGTTGGCAACAACCTTCTCATTTTGAATAGAGTTTGTGTG
TACTTCTCCATATTAATTTATATGATAAAATAGGTGGGGAGAGCTGAACCTTAACTGTCA
TGTTTTGTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
CCAATATGTTGCAGTACACTATTGTACAGGCGTGGAGACTCATTTGATATGTAAGAATA
TTTTCTGACAGTGAGTGACCCGAGTCTCTGGTGTACCTCTTACAGCTCAGCTGCCTGGCAG
CAGTCATTTTTCTAAAGGTTTACAAGTATTTAGAACCTTTTACGTCAGGGCAAAATGTTT
ATGAAGTTATTCCTTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT
ATGTTCTGGAATAATTTTACAAAACAAGCTATTGTAGTTTTGACTTGCAGAGCTGACAAACA
TGACAGTGGATTCTCTTTACAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
TTTTTGTAACTAATCCTTTTATTGGTAAAAATGTAAATTAAGATGTCAACTTG

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FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

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FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTGGCC
 CCTTTGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCTGTGTTCCCTTGTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAACTCT
 GAGGGAAGTTCCTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAAAGAGAGCCACAGTGCACTTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGTA
 AATAATTAAGAACAATTTAACAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

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FIGURE 6

MAAEEEEDEVWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPPEPVILVACVP
LVFDDEEESKLTYTEIHQYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAADFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSdleHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLTKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

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FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATC²ACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAA

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FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGCGCTTCTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC
 AGTGGAAATGCGAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTCTTGTGCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCCTGGAAGGAATCTCTGATTTCATGAAGTGGTCCATTCTGCCT
 TTCTTTATTTCTGGATAACTTGATTGTCTTCTATGTCCCTGTCCATCTTCAACGAGCCATG
 GCTGTTATCTTCCAAATTTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGCTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTATTTTTGTCTATTGTGGCT
 TGACTCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCACAGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCCTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTGGCATGGGCCATGTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACCTCATTTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAGAAGCTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTCAGGGCCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGCTTGTATGGGCCAGGTACCACGTGCATTATACAAACAGTGTCTGCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAAGCCCATCAGTCTCTCTCTATA
 TTTATTTAAGTATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGA
 GCTCTCTGAACCTTATTTTCACATTTTCAGTGTTTGAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCTAATATTTCTTTGCATATATCTAGCTACTCCCTAAATGGGT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAACCTGTAATAATCATGTTAGCTATAGCTTGATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 CTCCCTTTTAAACATTATAAAGCTAGGTTGTCTCTGAAATTTTGGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCTTTCTAAAGACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAAATATTTTGTGAAGAAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTTGATTTTGT
 AATAATCTTTTGTATGTTTAAACATTTGGTTCCTTAGTCACCATAGTTACCACTTGTATTTTA
 AGTCATTTAAACAAGCCGCGGTGGGCTTTTTTCTCCTCAGTTTGAAGGAAAAAATCTTGAT
 GTCATTACTCCTGAATTATTACATTTTGGAGAATAAGAGGGCACTTTTATTTATAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCAAGAGTTGAAATGCTGGCTCAGAATCATAC
 CAGATTTGTCAAGTGAAGCTGATGCCCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGAC
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGAGTGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATAA
 AAATTAGCAACAAGAGTACTTGTCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGGCAGCCTGTATGTTTACAGACTACCATCTGTAATATGACCTTATGTGTG
 CATCTCAGAACTTATACATTTTCTGCTCTCTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTCATTTGTGATATCCCAATAATATGACTGGCAAGAAATG
 GTGGAATTTGTAATTTAAATAATTTTAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPMAMAV
IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAAF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSASFVALI
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGTGAAGAGCGCTCAAA
CTGGATCCAGTGGGCTTCCTCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

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CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGCGGCC
TGGGCTAAGGCTGCTACGAAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGACGAGGACGAT
CCCCCTCTACAGGTCCCAAGCGCGCTGGCCGCGGGTGTGCGGCAAGGAGAAGGCGCGAG
AGCGGCTCCGCGGCGGGGCTGCTACCCACGAGCATCTTCAAAGCACTGAACGCCCGGCCCA
GGTAGAAGAAAGAACGAAAAGAGAAACACAGATTGCTGTGTGCAACCAAGCTTGTCTATG
CACTTGGGGGAGCCCCACAGGTGACGGGCTGTGCCCTGGGTTTCTTCTCTCAGATTAC
CTATTGCAATGGCTGAGTTCAGTTCAGGCTCCCTTTCTCTGCTTCATCACTCTGTTTGTGGGCGGAG
CTGGGATGCCATCAGACAGCCCCGGTGGGCTCTGCATCAGCAATCCCCGTTGGACCTGCC
TGGGTGCGCTTATGCGCTGGATCATCTTCTCCAGCCCCGTGGCGGTTCATTGCTACTTCTCT
ATCTGGTTGCTGCGGCACTCCCAACGCGGACACCTATTGGTACTGCTTTTCTATTGCTCT
CTTTGAACAATGCTACGTTGTTTTCATGTCTTCCATCTCGGCTCTACCACTGTTCATCAGCA
ACCGAGCAGACTGACGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTCTGGGAC
AGTGTGGGACGCGCATCAGGGACAATCTGGTGGCCCAAGCAGACGCGCTTGTTCAGG
ACTTCAATAGCTCTACAGTAGTCTCAAAAGTGCACCACTACATAGGACCACTTCCAC
AGGGAACCGCAAAAGGCATCTGCTGCGGACGCGGGGTTCATTGTCTGTATCTATATATCTG
TGCTGTATCTCTGATCTGGGCGTGGGAGCAGAGAACCCTATGAAGCCGACGAGTCTG
AGCAATCGCTACTTCCGGGCTTACGGCTGGTCATGAGCCACGGCCCCATACATCAAATT
ATTACTGGCTTCTCTTCACTCTCTGGCTTTTCATGCTGGTGAGGGGAACCTTGTCTGTT
TTGACCTTACCTCTGGGCTTCGCAATGAATTCAGAACTTACTCTGGCCATCATGCTCT
CGGCCACTTTAACCATTTCCATCTGCGAGTGGTTCCTGACCGGTTTGGCAAGAAGACAGT
GTATATTTGGGATCTCATCAGCAGTGCCATTCTCATCTTGGTGGCCCTGCTGAGAGATA
CTCATCATCATATAGTCGGTAGCTGTGGACGTGGCATGAGTGGCAGCTGCCTTCTTAC
TACCTTGGTCCATGCTGCTGATGTATTACGACTTCCATCTGAAGCAGCCCCACTTCAT
GGAACCGAGCCGCTCTTCTTCTTCTTCTTCTTCTTCAACAAGTTGCTCTGGAGTGT
ACTGGGCATTCTTACCCTGACTCTGGACTTTGACGGGTACCAGACCCGTGGCTGCTCGCAG
CGGAACGCTGCAAGTTTACATGAACTGCTGTCGACCTAGGCTCCCATAGTTCATCTCTG
CTGGGCTGCTGCTGCTTCAAAATGATCCCACTGATGAGGAGGCGCGCGAGATAAGAA
GGCCCTGCAGGCCTGAGGCGAGCGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
AGCTTGGCTAGCATCTCTCTAGGCGGCCACGTTGCCGAAGCCACCCTCAGAAGGCCACAG
AAGGATCAGGACCTGTCTCGCGCTTGTGAGCAGCTGGACTGCAAGTGTAGGAAGGGAA
CTGAAGACTCAAGGAGGTGGCCAGGACACTGCTGTGCTACTGTGGGCGCGGCTGCTCTG
TGCCCTCTCTGCTCCCTCTGCTGCTCTGTGGGCGAAGCCTGGGCTGCCATCTGTGAATA
TGCCAAGGACTGATCGGGCTAGCCCGGAACACTAATGTAGAACCCTTTTTTTTACAGGCC
TAATTAATAACTTAATGACTGTGATACATGAACATGTGTGTATGTATGTCTGTGAGCTA
TTAATTCTTATTAATTTTACATAAAGCTGGAAGG

FIGURE 12

MWLRWALS LPPSSCLWAEFGMP SQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGT EPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

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FIGURE 13

GGGAAACGAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGCCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

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FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGTCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
ACTTTCATTGTGGCAAACCTTCAGAAAACAACCCCTTTTGTCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCCTTTCACCAAATG
CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTGGGACTG
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTGATGAAGGAT
AAAAATTTCTGTAATGATTATGATTCCTCAGGGATTGGGGAAGGTTACAGAAAGTTGCTTA
TTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
TTAAAAACCTATGCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

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FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLRSRDI

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FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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CCACGACGCTCCGCCGCCCGCTGCGTCCCGAGTAGCAAGTGAGCTTCTCGGCTGCCCGCGGG
CCGGGGTGCAGGAGCCGACATGCGCCCCGCTTCTCGGCTCCTTCTGGTCTTCGCCGGCTGCAC
CTTCGCCTTGTACTTGTCTGTCAGACGCACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
AGGCTGGAGGCAGGTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTCGGGAGCTCTCTGAG
GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCTGCTCTTCTGCGGCGCCTA
CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTCTGATAAAGT
GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
TGAGACTTTTCCCATGACACCAAACCTGTTTCTGAACTCTCGGCCCAATTCTGAACATT
CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCTCTGTGT
GCAGACAGGGTCCATCCTGTCAACCCATAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCTCATTAATAAATTT
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
CACATGACTCTGGATTTTCTGTTTGCCACATCCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
TGTTGCTCCTAAAGCCCCCTCATGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGT
TTTCAAACACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCCTAGCAAAATCGTGTGTTG
GGCCGGGCGCGGTGGCTCAGCGCTTAATCCCAGCACTTGGGAGGCGCGAGCCGGTGAATC
ACAAGGTCAAGGATTCAAGACAGCTGTGCCAACAGATGGTGAATCCTGTCTTAATAAAAAAT
ACAAAAATTAGCAGGCTGGTGGCAGGCACTGTAATCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCCT
CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSGATCCYLLSS
IFGKQLVVSYPDPKVALLRKVEENRNSLFFLLFLRLFPMTPNWFLNLSAPILNIPVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

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FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGAC**Atg**GATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTCCTCACTCACCTGCCATTTCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGCTG**TAG**GAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAA

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 1066

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTHQCGMSEKAIEKFIRQLLEKNEPQRPPQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEFVLSGAHTWRSLSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPPYPWRRPLNRSQMLRELFPV
FTHLPFPKDasLNKCSFLHPEFVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 21

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

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FIGURE 22

CCCACGCGTCGCGCCACGCGTCCGGGTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGGTGGTG
 CCACTGGTGGCAGCGTCTAGACCGTGCCATGAGCCGTGGGGCTGCAGTGGGGACTGCC
 CCCCCGTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTGTGCCA
 CCCCCAATTGGCGCCACTTCACTCGACAAACAGGTACAGCCAAACCACTGCCAGTTCGAAATG
 GACACGTATGCTAAGAGCCAGCAGCTTATGTACGTTTCTGGAATGCCTGCTATGACATGTG
 TATGACAGTCGGGACGCGGCCAGTGGGAGCGCGCCAGAGTCGTCTGGGCGTTCCAGGAGC
 TGGTGTGGAACCTGGCGAGAGGCGGGCGCGCTGGAGGGGTACGCTACACGGCAGTGCTG
 AAGCAGCAGCAACGAGCAGCTCCATGGCCCTGCTGCACCTGGGGGGCGCTGTGGCGCCAGT
 CGCCAGCCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAACACTGTCCA
 GCGCCGAGACATATTCACGCATGCGGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTCAC
 CTGGAAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTGACACCCACCGAGGAGGC
 CTCACCTGCTCTGGCAGTGACCAAGAGGCCAAAGTGACCTGCCAGTTCGCTGCGAGG
 AGGACAGCTCGGCGAGGACGAGCTGGCTGAGCTGGGACCCGATGGAGGCGAGCAACTG
 GATGAGCAGCTGAGAAGCTGGTGCTCTCGGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCAGGCTGCTGGAGCTCACCACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 CGTGGAACACCGAGGAGGCATCGGCTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGAG
 GTCCACCTGGCGGCTTTCAACCTGCGCCGTTCAAGCACTTGAGCTTCTTCTATCTACAGGC
 CAACTACTTCTCAACTTCCCATGCAAGTGGGCAGCACCCAGTCTCATCTCTAGCCAGA
 CTCGAGACCTCCAGCTTGGCCCCATCCACCCATACCCAGGTACGGAACCCAGGTGTACTG
 TGGCTCTGCTGGCTTACGGCCCTCTCAAGGCTTACCAAGCAGCCGCTCCCCAGGAGTAT
 GCTGCTGCTGCTCAGGCCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTTCAGTACT
 TGATGCAACTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCACTACCTGTGTTCT
 CCTGTGCTCTGCGAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGGCGCTTCTCGG
 GGACCTCTCTAAGCCCTACGCTGTGGTGAACCCCAAGCATGCCACTCGTGAGGGAGAATG
 ATGAAGCTTTGAGGAGCAGCAGGACCATTGACAAGTTCCACTATGGCAGCCCACTACTCC
 AATGCAGCAGCGCTATGCACCTACCTCATCGCGTGGAGCCCTTCACTCCCTGACGTTCCA
 CTGTCAAAGTGGCCGCTTTGACTGCTCCGACCGGCGAGTTCACCTCGGTGGCGGCGAGCTGGC
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTACTTTCCCT
 GACTTCTCGGAGAACAGAACCGGTTTGAACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGCTGGGCCAGCTCTCTGAGGACTTATCCAGCAGCACCCGCC
 AGGCTCTGGAGTCGGAGTATGTGCTGCAACCTTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCGAGGAGGCCCTCAATGTCTTCTATTACTGCACTATGA
 GGGGGCTGTAGACCTTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTGA
 TCAGCAACTTTGGGCAGACTCCCTGTCACTGTCTGAAGGAGCCACTCCAACCTCGGCTCTCA
 GCTTGAGGAGCAGCCCATCGCCTTGCAGCCTGGACACTAACTCACTAGCATCTTCCAGCA
 CCTTGGAGCAACTCAAGGCATTCTTCGAGAGGTGACTGTGAGTGCAAGTGGGCTGTGCGGGA
 CCCACAGCTGTTTGCCTATGACCGCAACATAAGCAACTACTTCACTCTCAGCAAGAGCCCC
 ACCATGGGCAAGCCAGAGCAGCGACTGCTGAGTGGCCGCTGGGTGCCAGGCGAGTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTCAAGCGGTGGCCACTGGG
 ATGGCACTGCTCGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACTGCTGCTGCACTGGACACTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCAAGCTACGTAGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTGCTAGGCGCTGGCAG
 CAAAGCCTGTGCAAGCTCCTGTATGGGCAATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACCTGACATGGCTGTGCTGTGATCTGAGGATGGAATGTGATCATACACACTGTACGCGG
 CGGACAGTTTGTAGGGGCACTACGGCCTCTGGGTGCCACATTTCCCTGGACACTATTTTCCACC
 TGGCAATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGCTGGGAAGCTCCTGGGGCC
 CAGGTCACTACTCTTGCACCTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGCCCCCT
 GGCAGAGCAGCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCAACCGCCAGCTG
 GCGCCCTGCACTCTCCAACTAAACACACTGCTCCCGGCCGCGGCTCCTTGTGCCATGGAAG
 GTGGCCATCCGAGCCTGAGCGTGACCAAGGAGCGCAGCCAGCTGCTGTGGGCTGGAGGA
 TTGGCAAGCTCATCTGCTGGTGGTGGCGGGGCGAGCCCTCTGAGGCTGCGGAGCAGCTGTCGCG
 GGAAGCTGTGGCGGCTGCTGCGGCGCATCTCCAGGTGCTCTGGGAGAGAGCGGAATAACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCCGCGAGCCGTG
 GCGCGGAGGCCCCGCGGAGAAAGTCGGCGGGAACACCCGGGTGGGCAAGCCAGGCGGTGA
 GCGGGGCCACCTGCCCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCCGCCCTCGCCGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGCT

MSQFEMDITYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEFAQRRARLEG
RYTAVLKKQATQHSMAALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRCLKLPN
HHFDPHLEASALRDLNLEGEVPLTPTTEASLPLAVTKEAKVSTPELLQEDQLGEDELALETP
MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
RNQVYSWLLRLRPPSQGYLSSRPQEMLRASGLTQKWVQREISNFEXYLMQNTIAGRTYNDL
SQYPVPFWLQDYVSPPTLDLSNPAVFRDLSSKPIGVNPKHAQLVREKYESFEDPAGTIDKFH
YGTHYSNAGVMHYLIRVEPFTSLHVQLQSGRDFDCSDRQFHSVAAAWQARLES PADVKELIP
EFFYFPDFLENQNGFDLGLCLQLTNEKVGDDVLPWPWASSPEDFIQHRQALESEYVS AHLHEW
IDLIFGYKQRGPAEEALNVFYCYTYE GAVDL DHTDERERKALEGII SNFGQTPCQLLKEP
HPTRL SAEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
SFSKDPTMGSHKTRQLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLL
SQLSCHLDVVTCALALDTCGIYILISGSRDTCMVWRL LHQGLSVGLAPKPVQVLYGHGAAVS
CVAISTELDMAVSGSEDTGTVIHTVRRGQFVAALRPLGATFPGPFIH LALGSEGGIIVVQSSA
WERPGAQVITYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQNTLLPAA
PPLPMKVVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQLVSS
GETEYNPTEAR

amino acids 677-681

amino acids 985-989

amino acids 56-65, 367-376, 543-551

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGCCCCACCTTGTGAACTCCTCGTGCCCAGGGCTGATGCGCTCTTCAGGGCTACTCAT
 CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
 TGGACCTTAACGGGTACTGGCCCTGGGCCAATGCGTCCCTCGCTGGAGCCTTTGCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
 ATAGCCCGGGTCACTCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCCTCTGGTGTCTGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTGTCTGAGCAAAAGTACAGA
 CCTGTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTCTTT
 TTTTCTCCGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCCATATGTCATCGCCAGCGGCTTCTTCAGCGT
 TTTGCGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGACAACAAGAAGAGGAAGAAGTGAAGCAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGTTTTAGGCCAGGCGCGTGGCTCACGCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGTTGGCATGCACCTGTCATCCCAGCTAC
 TCGGAGGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLG
LFWTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTTCGTGTCGGATTTCGCGAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCTTGTTTC
 CAGTGTGACCCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAAGTTGAACTGTC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTGCTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGACGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCG
 CCACGTTTCCCGCCACAACACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCCCTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCTTTGTGTGTTGACAAAGAACCAGGCGCTGCAAAGCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAAGGCAGCGGAAGACACAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCTTAGGAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

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FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQPHYFILINCGANVDLLDILQPDEDITFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMG LPLKQVKQKFQAMD ISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGI PPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

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FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

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FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACCAGAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAGAGACAGTTTTTTTGGAAAGCTAA
 GCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATT
 GAGTAAAGTAGCTCCCGTCAACAATGGGTGACAGCCGCTGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCCGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC
 CAGCGCTGCCAACGGTGTCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAG
 CCTCTTCTCCGCGCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATC
 CTGAAGGGTGACAAGGGGACCCAGGCCAATGGGCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAAGCGCTTCTTCGCCCTTCTCAGTGGGCGCAAGACGGCCCTGCACAGC
 GCGCAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGGCACCGGCAAGTTTGTCTGCTCCCTGCTGGCATCTACTTCTTACGCTCAATGTGC
 ACAGCTGGAATTACAAGGAGAGCTACGTGCACATTATGCATAACGAAAGAGGCTGTCTC
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGGACCGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCAGAGACGCCATCTCACGCA
 ACGACTTCGACACCTACATCACTTCAAGCGCCACCTCATCAAGGCCAGGACGACTGAGGG
 CCTCTGGGCCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTCTGTGAAGCAGGAAGGCCAGGGAGGTCCCGGGGACCTGGCATCTCTGGGAGA
 CCGTCTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCT
 TGGACCTATTTTAAAGACTTGTAACTTAAATTTCTAGAATTTCCAGCCTCGTAGGCC
 AGCACTTCTCAAATTTGGAATGCATGCAATACCCGGGGTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGCTTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACTGGAGCAACAGGTTCTAGGACTTTCTCAATATCTTAG
 TACTTCTGAACATTTCTGGAATCTCCCCACATTTCTAGAATTTCCCAACATTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTCACTGC
 AACCTCTGCCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCTGGCTAATTTTTTGTATTTTTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTGGCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAAT
 CTGGGGATACAGGTGTGAGCCACCGTGCTGGCCAAATTTCAAACATTTCTTAAATTTCTCTAT
 CCTCCAGGGCTCCCGTGCTATGTTCTCTTTACCCCTTCCCGCTTCTCTTGTCTCAGGCC
 TGCACCCTCAGCCACCGTTTCAATTTATTCATTATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGTGAGGGGGTCAGACACAGGCCCTGCCCTGCCCTCAGTCACTGGCCA
 GTCCAGCCACGCGGGGAGAGATGTGTACATAGGTTTAAAGCAGACCCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTTCAAGTGCTGCTGCTCCTCATTACCACTGCCTCCCAAGGCTGG
 TGGGACGGGTCCTGGTGGCAGGGGCAAGTATCTCCTTCCCGTTCTCATCCACTGCCCCAG
 TGCTCATCGTTACAGCAAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCAATTTGGGGGGTGAAGTGGCCCCGAGAAATGGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTTGCAGAGAAGACCTTGCCCTCCTCAGTGGGATCCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCTTGTCTCAGTCCCTTCCACCAAAGTCACT
 GAACCTCGGTTTTCCAGAGGCCCTCAGCTGCCCTCAGACACTGATGTCTGTCCCGAGTGCT
 CTCTGCCCTCATGCCCCCTCTCACCGGCCAGTGGCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCCGGTGGGCGAGCTCTCGTCTCAGAGCCCTCCCGGCTGGTGGTCTGCTTTAC
 AAACACTGCAAGGAGAGGGCCACGGAAGCCCGAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGGAGGACCTCAGGCCTTCCGTTTCTTCTCCAGGGTGGGGTGGGCTGGT
 GTTCCCCTAGCTTCCAACCCAGGTGGGCTGCCCTTCTCCCCAGAGGGAGGGGCGGCTCCGC
 CCATTGGTGCTCATGCAGACTTGGGGCTGAGGTGCCCGGGGGTATCTCTCTGGTGTCTCAG
 AGCCGAGGGGAGCGGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
 AGACTGTGCTATAAACACCCTGCCCTGATCCTGCCCTGCTGACCCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGAATGCTGCTCCTCTTGAAAAAAGGAAAAA

FIGURE 30

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGMPGLPGYMGREGPGQGEPPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAAGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG
 AGGCCGCGGCTGCCCGCCCGGCTCCCTGCGCGCCGCCGCTCCCGGGACAGAAAGATG
 CTCACGGGTCCCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG
 GCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGCTTCTGCACGTGCCCGCCAGGGG
 ACCACGCTGCCCGAGACGTGCCACCCGACACGCTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGACCGAGGACGCTTTGCCGGCTGCCGGGCTGACGCTCCTGGACCTGTAC
 AGAACCAGATCGCCAGCCTGCCAGCGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAAAGGCTGCATGAAATCAACATGAGACCTTCGCTGGCCTGCGCGCCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACG
 TCAGCCGCTCTGGAGCTCAAGCTCGAGGACACAGAGCTGCGGGCACTGCCCGGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT
 CCTGGACACTGCCAACCTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACAC
 CGCATTTGCCAGCTGCGGCCGAGGACCTGCGCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCTGCTGCTGGCAGCTCTCGGGCTCTTCCCGGCTGCGG
 CTCTGCGAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTGGGCCCTG
 GGTGCGCGAGAGCCAGTCAACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCA
 AGAAGCTGGCCGGCTGCTCCTGGAGCTTGAATACGCCGACTTTGGCTGCCAGCCACCAAC
 ACCACAGCCACAGTGCACACACGAGGCGCTGGTGGGGAGCCCAAGCCTGTGCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCCTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGCCACCACTGGCGTGTGTGACCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCTACACCAAGTCA
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCACTCCCTGCGC
 GTGGGCTGCAGCGCTACCTCCAGGGAGCTCCGTGCAGCTCAGGAGCCTCCGCTCACCTA
 TCGAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCT
 AGTACACGTTACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCATGCTTTGGG
 CCGGGCGGGTGCCGGAGGGGAGGAGGCTGCGGGGAGGCCATACACCCAGCCGCTCCA
 CTCACACCGCCCACTACCCAGGCCCGCGAGGGCAACCTGCGCTCCTATTGGCCCG
 CCGTGGCCGGGTGCTCCTGGCCGCTGCTGCTGCGGTGGGGGAGCCTACTGTGTGCGGCG
 GGGCGGGCCATGGGACAGCGGCTCAGGACAAGGGCAGGTGGGGCCAGGGCTGGGCCCT
 GGAATGGAGGGAGTGAAGGCTCCCTTGAGGCCAGGCCGGAAGGCCACAGAGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGGCTGGCCTC
 CAGTCAACCCCTCCACGCAAGCCCTACACTAAAGCCAGAGAGAGACAGGGCAGCTGGGGCCG
 GGTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACACGTAAGTTCTCAGTCC
 CAACCTCGGGATGTGTGCAGACAGGCTGTGTGACCACAGTGGGCCCTGTTCCCTCTGGA
 CCTCGGCTCCTCTGCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACCTCCCAAGAAC
 CGAGTGCTATGAGACAGTGTCCGCCCTGCCCTCCGCAACGTGAGCTCCTGGGCACGGCG
 GGCCTGCCATGTGCTGGTAACGATGCTGGGTCTGCTGGGCTCTCCACTCAGGCGGA
 CCTGGGGGAGCTGAAGGAAGCTCCCGAAGAGCAGAGGAGCGGGTAGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAACTCAGAGACAAGGATTTGGTTTTGTAAGACAACGATGATATG
 AAGGCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAA

FIGURE 32

MCSRVP LLLPL LLL LALGPGVQGCPSGCQCSQPQT V FCTARQGT TVPRDVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDL SHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRRLLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
PWVRESHVTLASPEETRCHFP PKNAGRLLLELDYADFGCPATTTTATVP TTRPVVREPTALS
SSLAPT WLSPTAPATEAPSPPTAPPTVGPVPQQDCP PSTCLNGGTCHLGTRHHLACLCP E
GFTGLYCESQMGQTRPSPTPVTPRP PPSRLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRL
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMP LGPGRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGP GAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFFPGPLQSP LHAKPYI

0000732 11001

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATTCATTCATATGAGGAATAAGTGGTAAAAATCCTTGGAAAAATCAATGAGACTCATCAG
 AAAAATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCTCCAACTGTCTCTAAGAAAGGTTTCCCGCAGACTTGG
 ACCCCAACTCAACAGCACTGGATTATCCTATAACCTCCTTTTAAAGTCCGAGATTTCAGA
 TTTTCATTCTGTCTCCAAACTGAGAGTTTGTATTCTATGCCATAACAGAAATCAACAGCTGG
 ATTTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTGTCTAAATAACAGACTG
 AAGAGTGTAACTTTGGTATTTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAAATGACTT
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAAATCAAAAAATCAGATTTCCAGAAAAATTGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGTAGCCTGCCATCTTAAACACAAAC
 AAAACTGCACATTGTTTTACCAATGGACAAAAATTTCTGGGTCTTTTGGCGTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAATTTGTAAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGA AAAATGCTAAGACATCGGTTCTATTTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACTAT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
 TC AAAATCTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGGATAAAATCTATTGTCTTTTGACCAAAATGGACATAGAAAACCTGACAAATACAAATG
 CACAAATGCCACACATGCTTTTCCC GAATTTCTCTACGAAATTCAAATTTTAAATTTTGGC
 AATAATATCTTTAAACAGACGAGTTGTTTAAAGAACTATCCAATCGCCTCACTTGAAAACCT
 CATTTTGAATTTGGCAATAAATGGAGACACTTTCTTAGTAAGTTGCTTTTGTCTAACACACAC
 CCTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTTGCTCA
 TGCCGAGAACTGTGGTCAATATGAATCTGTCTACAATAAATTTGCTGATTTCTGTTCTCAG
 GTGCTTGCCCAAACTGATTTCAAACTCTGACCTTAAATTAATAACCAAAATCCAACTGTACCTA
 AGACAGACTTAATCATCTGATGGCCTTACGAGAACTAAAATTTGCAATTTTAAATTTTCTAAGTAT
 CTCCTCGGATGCACTCATTTTCACTAGACTTTCAGTTCTGAACATTGAAATGAACTTCTATTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAAACTCTAAATGCCGGAAGAA
 ATCCATTCGGGTGTACCTGTGAAATTA AAAATTTTCATTCAGCTTGAAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTATACACCTGTGAATACCCCTTAAACCTAAGGGAACATAG
 GTTAAAGAGACCTTCATCTCCACGAATTTATCTGCAACACAGCTCTGTGTGATTTGCACCAATTTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAAACACCCA
 AGAACAACCTCAAGAGAAATGTCCGATTCACGCATTTATTTATACAGAGTGAACATGATTTCTC
 TGTGGGTGAAGAAATGAATGATCCCCAATCTAGAGAAGGAAGATGGTCTGATCTTGATTTGCT
 CTTTATGAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATTGTAAAGCTTCAATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTTGGCCACCACAATCTCTCCATGAAAATTTCTGATCATATAATTTCTTATC
 TTTACTGGAACCCATTTCCATTTCTATGCAATTTCCACAGGTTATCATAACTGAAAGCTCTCCT
 GGA AAAAAGACATACTTTGGAATGGCCCAAGGATAGGCGATGGGCTTTTCTGGGGCAA
 ACTCTCGAGCTGCTATTAATGTTAATGTTATAGCCACAGAGAATGATGAACTCGAGACA
 TTTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
 ATAAAAATCCACAGTCCCTGGGAAGTTGGGGACCACTACACTGTTGGGATGTACATTGATA
 CAACCTTTTGAATTTTGTAAATTTGACAATATTTATTA AAAATTA AAAATGTTTATTTCCCTCAT
 TCAGTTTCTAGAAAGGATTTCTAAGAAATGTATCCTATAGAAAACACCTTCAAGATTTATAAGG
 GC TTTATGAAA AAAAGTGTCTATCCAGGATTTGTTTATAATCATAAAAATGTGGCCAGGCTGC
 AGTGGGCTCACCTTTGTAATCCAGCACTATGGGAGGCCAAGGTGGGTGAGCCACAGAGGTCAA
 GAGATGGAGACCATCTGGGCCAACATGGTGAACCCCTGTCTCTACTAAAAATCAAAAATTA
 CTTGGGCGTGATGGTGCAGCCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCGAGGAAATCG
 GTTGAACCCGGGAGGTGGCAGTTGCACTGAGCTGAGATCGAGCCCATGCATCCAGCTGGT
 GACAGAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGTGA AAAACATCC
 TCATGGCCACAATAAAGTCTAATTCATAAATTAATAGTACATTAATGTAATATAATATTA
 CATGCCACTAAAAAGAAATTAAGGTAGCTGTATTTTCTGGTATGAAAAAACAATTAATAT
 GTTATAAACTATAGGTTGGTGCAAAACTAATTTGTTTGTGCAATTTGAAATGGCATTTGAA
 ATAAAAAGTTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGGGAGGTGGA
 TTACAGGAGCATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATTTGTTAGATGA
 ATCTGTATTTCTTTTATAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

MRLIRNIYIFCSIVMIAEGDAPELPEERELMTNCSNMSLRKVPADLTPTATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIOQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPMICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDLGDKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVLDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKYILLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLTSLVSCFANNTPLEHLDLSONLLQHKNDENCSPWETVVMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTPKETIHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLEYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMVLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKTTOEQELKRNVRFHAFITSYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSIENI
VSFIEKSYKSFVLPSPNFVQNEWCHYEFYFAHHNLFHENSDDHILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCKGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

GGGGCTTCTTTGGGGCTTTTGCTTGGAAACACTGCCTCCAAAGGACCGCGCTCGAGGGGTTGCGGGAAGGCGG
CGAGGAAGAAGGAAGGCGGGGCGGGCCCTCGCGCGCGCGCGCGCTTCGCGCGGCTCTTCGCGCGGCGG
CCAGCCCAACCGCAGCCCGCGGGCGGTCACACGCGCAGCAGCGCGCGCTCCGCGGCCACCGCGCGCTCT
CTGCTGTGCTCTCGCGCTTGGCCGCGCGCAGCTTTGCGCGCGGCGCGCGCGCGCGCGCGGCGTGAACGTGA
CCTTGCCCTTGGGCGCGGGCGCAGCAGCAGTGGTCCCGCGGGGACCGTACCACCGCTTGGCCCTGGTGTCT
CTGGCAGTGAACCTGGCGGGGTGGAGCGCCAGGGGCGAGCCCTCGAGGACCTGATTATTCGGGCGAGGAT
CTGGAGCGGGAGCCCTATACGCGCGCGGGAGCCGAGCTCGAGACCTTCTCTCGCGCTGCCCTCGCGGGC
CCGGGAGGAGATGGGAGCGCGGCCCGAGGAGCGAGCGCCGCGAAGGGGACCAACCGCCCAAGAAGCTCG
AAGAGAGGAGAGTGGCTCGGAGCGCGCTCCACAGGTTAAACACGACGAAACAAAAAGTTATGACACCAAGT
CTCTGAGAAGGCTGCCACGATGATCAGAGTGTCTGGTGGTGGGCTGAAGATGTACACAGAGAGTTGGCCCTCT
TTGGTCTGGAAACCTTAAAACTACAGACTTCAGCTCTCAGCTGCTCACGGTGACCGGTAAGCGCTTATGGCTTGGGGCA
TTCAGGAGGACACTCACATCGAGGGGCAATGATAAAATGATTTTATGACGAGGCTGGTGTGCGCGGAGG
AATACGCTCCAGCACTGGATTGAAGTGAGTGTCTGGCGCTCGACGAGTCACTGGTCTCACTCACTCAAGGAG
GGAACCTCCCTCTGCTGAGTGAATCTGGTGTGATCCTATAAGTCACTGGTAGAGATGACAGGCCACCTGGGT
ACTGTTAAGATAGTCTTGGAGACATGATTTAGGAGGAAACAGTGAAGAAGAGTACCTGTTTCTAATGAGCT
ACCCCTCCCAATGGTGGCCCGCTACATCCGCTAAACCCCTCAGTCTGGTTTGATATGGGAGACATTCGATGA
GAATGAGATCTGGGTGGCTGCCATCGAGATCTAATAATTATTAACCGCGGAAACGAGATGACCCACATCT
GATGATCTGGATTTTAAAGCACCAATTAAGAAGATGCGCCAGTGTGAAGAAATGTGAATGAATGTGTCC
CAATATACACGAATTTAAACAATTTGAAAAGGACCAAGCGGCTGAAGCTGTATGCTGTGAGATCTCAGTCT
ACCTCGGGGAGCAATGAAGTCTGCTGAGCCGAGTTCACATCACTACGCGGGGGCCACGGCAATGAGGTGTCTGGCG
CGGGAGTCTGTGTGCTGTGGTGAGTCTGTGTGTGAGAGTATTTGGCCGGAAATGCGCGATCGTCAACT
GGTGGAGGAGACCGGGAATCGGCTCTCCCTCCCTCCCTCAACCCGATGGCTACAGAGAAGCCTCAGAGAAGGGCT
CGGAGCTGGAGGGCTGTGCTCTGAGGACCTGGACCGGAGTGAATGACATCAACAACAACTTTCTGATTTA
AACACGCTCTCTCTGGGAGCGAGAGATCAGACAGATTCGCCAGAGAAAGTTCCCAATCACTATATCACTACCT
TGAGTGGTTTGCTGTGGAATAATGACAGGTGGTCCGAGACAGGAAGCAGTCACTAGCCTGGATGAAAATAATCC
TTTTTGTCTGGGCGCAACTCGAGGCGCGGAGCTGGTGGGCGATTCCTACAGCCTTGGTGGCTCCCC
TGGAAGAGGAGGAACACACCCCAACCCCGATGACAGTGTCCGCTGGTGGCTACTCTATGCTTCCAC
ACACCGCCTCATGACAGACGCGCGGAGGAGGCTGGCCACAGGAGGACTTCAGAGAAGGAGGAGGCACTGTCA
ATGGGGCTCTCTGGCACACGCTCGCTGGAAGTTGAAAGACTTCAGTACTCTTCAACAACTCTCTGCAAGT
TCCATCTACGTGGGCTGTGATAAATCCCACTAGAGCGAGCTGCCGAGGATGGAGAAATACCGGGAATCT
TCTGATCTGTTCTATGAGCAGGTTTCTGTGCGATTTAAAGGCTTGTTGATGAGATTCAGTGAAGAAATCC
CAAAGGCCATATGATCTCGTGAAGAGCAATTAACCTAGACTCGGAACGCAACGAGTGGGATTTACTGGCGCTCT
TGAAACCTGGAGAGTTATGGTTCAGACGAAGCGGAGGCTTGTTCACTGATCCACAGAACTGTATGGTGG
CTGTACGATCGGGGCGACAGGCTGTACTTCACACTTACGAAAACCAACATGGCGAGATCGGAGACATGG
AGAAATTTGGAAGACCAACCTCAGCTCGGACCGAGGCGGCTGAAGCTCGGGGCGGAAAGACACAGCACTGG
GGTGCACCTCTCGGGCCTTTGAGCTGCTCTGGGCAAGTGCAAATTAACACAACTGCTGATGAGCTCATAG
TGAGTCACTCACTGTTGTTTCTGTGTAATCABAAGTCCGTTGAAGAGAGGCTGCAATTCAGCGAGCTCG
CAAAGAGGAGGCTGGAGGCTGAGGCTGTTTCTTTCTTTCTGCTCCATTTATCAAATTAAGCTTGGACAGGCA
CGAGAGAAAGCTGATGGAGTGAAGAGACTCAGAACGCAACCTGGGAATCAGAGAGAGGAGGAGGAGGAGG
GAGCTCTCGCTTCTGAGGCTCTGGCTGCATGAAGAAAGATCTGTGTTGCTTCCCTGTTTGGCTGGACAGAGG
TTTCCAGTGTGGAATTTGCAATTTGCACAGTAAATTTGAGCATTTCCCAAGTGGGCTGCCAAATGTTTACA
TTTGTGATGCTCCCAAGCGCTCTAAGAAATGCACCTCTCTGGCCCTGGGACATCGAAGCTGTACTCAATAAT
ATTTCTGTTCTTTGACATAGCCTCATTGCCAGTGCACATCAGTGAAGCTCTTGAATGTGTTTACTGCTCT
TTTTCAAACAAAGGAGTGTTGTCAPAAAGGAGGAGGAGGCTGAGATCACTCAGGATGTTTGGGCGACAGCA
TGAGGCTCTTGCACAAATTTGGGCTCATAAACACCGCCAAAGTCCCTGTGATTCAGTAGCCTGGAGGTT
CCCCAGTAGGAGGAGGAGGAGGCGGACCTCTCTGAAGGGCGAAATTTAGCCTGGATCTCTCTTTTAC
CTGCTAGGACTGGAAGAGGCAAGTGGGTGGCTTGAAGCCCTCTCTGCTGAGGATTTGCCCTGTGCTG
GAATTGAGTGTCTATGGTGTGGCTCATATACGCTGGAGTATTTTGTATGTGTAAGTGCAGATCTCCA
GATTAGGCTTAATGTAATGAAAACCTCTAGGATTACTTGGAGACTCAGTTTGGGAAGATTAATGAATTA
CTTGCAGAAAAAAGTATGTCTCACTTTTGTAAATGTGCTGCTCATTGACTGGGAAAAATGAAAAA
AATTAAGCAAACTGTAGACCTTTAAAAAABAAAAABAAAAABAAAAAABAAAAAABAAAAAABAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESC PPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLRTFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPD PNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNP DGYEKAYEGG
SELGGWSLGRWTHD GIDINNNFPDLNTLLWEADRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKI PFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYS YAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARI REIMEKFGKQPVS LPARR
LKLGRKRRQRG

0000772.11001

FIGURE 37

CTAAGAGGACAAGATAGAGGCCCGGCTCTCAITTTCTCCTAGCCCTTCTGTTCTCCCTGGCCAAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACTCCCAATTCACAGCCCGGCTTCAGCTCTTCCAGGTTGTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTGGGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCAGTTGTT
 TTCCAATTTTCCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTTTCCCTGCCAGACACACCTTTTC
 CCGTGACAGATGGAAAGCTTGGAAATCACAGCTCATGTTCTTTCTCAGAAAGTTTGAGAAAGAACTTTCTAAA
 CTGAGGGAATATGTCCAATTAATTAGTCTGTATGAAAAGAACTGTTAAACCTAACGTGTCGGAATTGACATCAT
 GGAGAGGATACCATTTCTTACACTGAAGCTGGACTGACGTGATCAAGGTGAAGGAGTGAAGGAGTGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATGTTGACAGCTGGAAGTGGAGATGAAGAAAT
 ATGACTCTTGGTAGAGAGCTTGAGACACTAGACAAAAACAATGCCTTGCCTTCCCGAGAAATCTGTGGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCTCTAAGATCAAAACACCCCTGTGCTCCACCTCTCTCCACTC
 CAGGAGCTGTGCTCATGGTGTGTTGGTGAACATCAGCAACCCCTGTGTTGCTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGTTGCTTGGGGTAGGGATTACTCTCCCGAGCTCCAAACAAAGGACTGATTTGGGTGGCGCC
 ATTTGAATACAGATGGGAGACTGTTGGAGATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCAAGGTAGTGGTACAGCAGTTTACAACACACACTGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCAACACAGATGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCTATAATAACCGCTTTTATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTTATCACTGAAGCCGACACTGGTAACTGTTGATTAGTAACTCAATGACACCACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCAACGCTTTCATGGTATGTGGGTTCT
 GTATGCCACCCGTACTATGAACACCAAGACAGAGAGATTTTTTACTATTATGACACAAACACAGGGAAGAGG
 GCAAACTAGACATTGTAAATGCATAAGATGCAGGAAAAAGTGCAGAGCAATTAACCTATAACCTTTTGACCAAGAA
 CTTTATGTCTATAACGATGTTTACCTCTGAATTAATGATCTTCTGCTTTCGAGAAAGCCCACTAAGCTGTTTA
 GGAGTTAGGGTGAAAGAGAAAAATGTTTGTGAAAAATAGTCTTCCACTTACTAGATATCTGCAGGGGTGT
 CTAAGAGTGTGTTCAATTTGCAGCAATGTTAGGTGCATAGTTCTACCACTAGAGATCTAGGACATTTGTCT
 TGATTTGGTGAGTCTCTTGGGAATCATCTGCTCTTCAGGCGCAATTTGCAATTAAGTCTGTCTAGGGTGGGA
 TTGTCAGAGGTGTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGGACTTAAAACTCAGTATGGCTGTAGGGATTCTTGTACAGGAATATTGCCCAATGACTAGTC
 CTATCCATGTAGCACCCTAATTTCTCCATGCTGGAAGAAACCTGGGAGCTTAGTTAGGTAGATTAATATCT
 GGAGCTCTCGAGGGACCAATCTCCAATTTTTTTTCCCTCACTAGCAGCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAGTGTCTGAGTTTATGAGAGAGGCGCTTTT
 ATGCATTAATTTGTACATGGCAATAAATCCGAGAGGATCTGTAGATGAGGCACTGCTTTTCTTTTCTCTC
 ATTGTCCACCTTACTAAAGTCAGTAGAATCTTACCTCATAACTTCTTCCAAAGGCAGCTCAGAGATTAG
 AACCAGACTACTAAACCAATTCACCCGCCCAACCCCTTCACTGCCCTATTAAAAAATTAATAGTTTTT
 CTATGGAACTGATCAAGATTAGAAAAATTAATTTCTTATTTTCAATTAGACTTTTATTTACACTCTA
 AGACTATAAGAAATCTGATGGCAGTGACAAAGTGCTAGCATTTATGTTATCAATAAAGACTTGGAGCAT
 TGTGCAACTTATGATGTATCAGTTGTTGCAATGTAATTTTTCCTTTTGGTTTAAAGCTGGAACCTGTAGAGAAAT
 GAAATTTAATTTTTTTCTAGGACGAGCTATAGAAAGCTATTGAGAGTATCTAGTTATCTGACGTGAGTAGT
 TGGAAACCTTGTGTTGATGTGATGTGCTTGTGCTTTGAATGACTTTATCATCTAGTCITTTGTCTATTT
 TCTTTGATGTTCAAGTCTAGTCTATAGGATGGCAGTTTAAATGCTTACTCCCTTTTAAAAATAATGAT
 TAAAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSFSSSSSRSGSSSSRSLGS
GGSVSQLFNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTFPVVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGlyWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMVNMNTGNIARVNLTNTIAVTQTLNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF
MVCGLYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

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FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAGATGCGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATTGTTTGTGTGAAGTGCCCGGTGTTTGGCTATGCCAGTGTCTCCTAGTGTGAAAC
 AACTCCACTGTAACTAGATGTATGCACTTTTCTTGGCTGTTGGAGTATGTGTAGCTTGT
 TGTAACTGTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGAGAAATG
 AGAAAGCTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGTTCTATCTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGACATGA
 TCCTAGAGCTGCACTGCAACAATGGATTTTGGTTCTTTAAATTTGCTGACAGCAATTGCAATTA
 TTATTGGGGCATTCTTCATTCAGAGGAACCTTTACAACCTGTGTGTTTTATGTAGGCATG
 GCAGGTGCCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTTGATTTTGCACATTCATG
 GAATGAATCGTGGGTGAAAAAAATGGAAGAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTAATCTGCTGCTTTAGTTGCTATCGTCCGTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTCAAGAAACAAAGCGTTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGTTGCTTCTGTAATGTCTATATCGCAAAAAATCCAAGAATCACAACCAAGATCTGGTT
 TGTTCAGCTCTTCAGTAATTACAGCTCTACACAATGTATTTGACATGGTCACTATGACCAAT
 GAACAGAAACAAATGCAACCCCAAGTCTACTAAGCATAATTTGGCTACAATACAACCAAGC
 TGTCCCAAAGGAAGGGCAGTCACTGCGTGGTGGCATGTCAAGGAATTTATAGGCAATTAATTC
 TCTTTTGTGTTGTGTTATTTTATCCAGCATCCGTAATCTCAAACAATGTCAGGTTTAATAAA
 CTGACTCTACAAGTGATGAATCTACATTAATGAAGATGGTGGAGCTAGAAGTGATGGATG
 ACTGGAGGATGGGGACGATGTTCCAGGAGCTGTAGATAATGAAAGGATGGTGTCACTTACA
 GTTGTCTCTCTCTTCACTTCTGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC
 AACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAAGTCACTGGACAGCTGTCTGGGTGAA
 AATCTCTCCAGTTGGATTGGCATCGTGTATGTTTGGGACACTCGTGGCACCCTTTGTTCT
 TTACAAATCGTGATTTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTATTGC
 TTTTGTGAAACAGTATCCCACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAAC
 TTCTCCAGTGTCTCGCATGAATTAGATTTTACTGCTTGTCTATTTGTTATTTCTTACC
 GTGCATTTGATATGAGTAGAATGAATTTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT
 TAGTAAAGTGGCCATTTATTTGGGCTTATTTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAATTTGTTTGAATTTTAAAAATATATTAGACCTTAAAGCTGTTTTAGCAAGCATTTAA
 GCAAATGTATGGCTGCCCTTTTGAATATTTGATGTGTTGCCCTGGCAGGATACTGCAAGAAC
 ATGGTTTATTTTAAATTTATAAACAAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGCAATAGTGTAGG
 TTAATGGATGGAGGTGTCCGTACTAAATGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGCCCTTTGCCAAACAAAGTGAAGTGTGTTGTTGTTTAAACTCATGAAGTATGGGTTCACT
 GGAATATGTTTGAAGCTGGAAGGATTTAGACAAGTTTTGAAAGGATAATCATGGGTTAGA
 AGGAAGTGTGTTGAAGTCACTTTGAAAGTTAGTTTGGGCCAGCAGCGTAGCTCACCCCTT
 GGTAAATCCAGCATTGTTGGAGCTTAAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTTGGCAGATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCTGTGGTCT
 CAGCAGCTGAGAGGCTAGTGAAGATTTGCTGAGCCAGAGCCAAAGGTTGCACTGAGCAAGTCA
 CGTCACTGCACTCTAGCTGGCAGAGATGAAGCCAAAAAATATATATATGAAATCAAGG
 AGGCAAAATTTGACAGGGAAGGAAGTAACTGCAAAATCCCACTAGGCTTTAGTAGGTACTTAT
 ATAAATCTAGTCACTCTCTCATTAAAAAATGAAGACACTGAAATACAGACTTAAATTA
 GTCAGATAGCTAATTAGGAATTTCAAGTTGGCCAATAATAGCATTTCTCTGACATTTT
 AAATAATTTCTATTCAAAATACATGATATTTGATTTACACCTCATAGTGTGATTAATTAATGT
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAATGATGGAATGTTT
 AGAATAAACCTCTGTTTATAGTATATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTAAGCCGATGTAATGAAATATATAGATTATTGTAACCTTTCAACCTGAAAACTCAAGCAGT
 ATGAGGTTTGAAGTTTATGATGTGTCTAGTGTCTAATGAGCTTTTAAATCTCAAAAT
 TCTTTTAAAAATTTTATTAATGTGAATGGAATATAACAACTGACGTTAATTTCCCAACC
 TTATCTGTGTGTAGACATTGTATCCACAATTTGATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

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FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFITVWFYVGMAGAFCFILIQLVLLIDFAHSWNESSWEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLNDRFD

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FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGCTCCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA
TGCAC TTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATAACCAGGAATGGAAG
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTGTTGNTATGCCGATGCTGTCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCCTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGTGTTGTCCCTTGTAACATTTTGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTATGGGGC

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FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTGGTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTCAGAAAACAAGGC
GTTTCATCAGTGTC AACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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FIGURE 46

CTCGGGCGCGCACAGGCGAGCTCGGTTTGCCTGCGATTGAGCTCGGGGTGCGCGCCGGCGCGGCCCTCTCCAAT
 GGCAAAATGTGTGTGGCTGGAGGGCGAGCGCGAGGCTTTCGGCAAAAGGCAGTGCAGTGTTCGACAGCCGGGGCGAG
 TCCCTGTGAAAGCAGATAAAGAAAACATTATTAACTGTCTATTACGGGGAGCGCCCGGGCGGGCTGTGCG
 ACTCCCGCGCGAACATTTTGGCTCCCTCCAGCTCCGAGAGGAGGAGAAAGCGGAAAGAGGCGAATTCAC
 TGTGTTTTCAGGCAAGTGGACATGTATGATGGCCCTCCTGAATTTATCAGATGTGTGATTTATAGCGATGCC
 CCTCGGTTTGTGTGTGTACGCACACACAGCTGACACAAAGGCTCTGGCTCGCTTCCCTCCCTCGTTCCAGCTCC
 TGGGCGAATCCACATCTGTTTCACTCTCCGCGGAGGGCGAGCAGGAGCGAGACTGTGCGAATTCGAGTCC
 AAGAGGGACGAGGGAAAAGAAAAGCCACAGACCACTTGAAGCTCCCGCATCCCAAAGAACACAGAT
 CAGCAAAAAAGAAAGATGGGCCCGCGAGCTCTGCTGTGCTTGTGCTCCCACTGTGTTCTCCCTGTGGG
 TGGAACTCGGCTTCTGTGCGACCCAGCGCTGAAAGGAGGTTTCAGAGGGACCCGAGGAACATCCGCCCCA
 ACATCATCTCTGCTGCTGACGGACAGCCAGGATGTGGAGCTGGGTTCCATGCAAGTGTATGAACAGAACCCGCGC
 AGGCACAGCAGAGAGCCGCACTTTGCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTGGGAAG
 TATCTTAATGAATACACCGGCTCTACGTGCCACCCGGCTGGAAGGAGTGGGTCCGACTCCTTAAAAACTCCCG
 CTTTATAACTACAGCTGTGTGCGAACGGGTGAAAGAGAGACAGCGCTCCGACTCTCCAGGATTACCTCA
 CAGACCTCATCAACCAATGACAGCGTGAAGCTTCTTCCGACGTCGAAGAGATGTACCCGACAGGCCGCTCTC
 ATGTTGATCATCGCATGCGACGCCCCAGCGGCTGAGGATTCAGCCCCACAAATTAACGCTCTTCCCAACCG
 ATCTCAGCACTCAGCGCGAGCTACAACTACGCGCCCAACCCGAGCAAACTGGATCATGCGCTACACGGGGC
 CCATGAGGCCCATCCACATGAAATTCACCAACATGCTCAGCGGGAAGCGCTTGCAGACCCCTCATGTCCGTGGAC
 GACTTCATGGAGACGATTACAACATGCTGGTTGAGACGGGCGAGCTGGACAAACACATACATCGTATACACCGC
 CGAACCGGTTACCATCTCGGCGCATTTTGGCTGGTGAAGGGAATCCATGCAATGAGTTTGCATACAGG
 TCCGCTTCTACGTGAGGGGCCCAACGCTGGAAGCGGCTGTCTGAATCCCACTCTGCTCAACATGACCTG
 GCCCCACCTCTGTCGACTTGCAGGCTGTGACATACCTGCGGATATGAGCGGGAATCCATCCTCAAGCTGCT
 GCACAGCGAGCGCGCGTGAATCGTTTCACTTGA AAAAGAGATGAGGCTGTGGCGGACTCCTTCTTGGTGG
 AGAGGGCAGCTGCTACACAAAGAGACAAATGACAAGTGGAGCGCCAGGAGGAGAACTTCTGCCCAAGTAC
 CAGCGCTGTGAAGACTCTGTGACGCTGCTGATACCAAGCGCGGTGTGAGCAGCTGGGACAGAGTGGCAGTG
 TGTGAGGAGCGCCACGCGGAAGCTGAACTGCATAAGTGAAGGCCCATGCGGCTGGCGGACAGCAGACGCC
 TCTCCAACTCTGTCGCCAAGTACTACGGGCGAGGCGAGCGCTGCACCTGTGACAGCGGGGACTTCAAGCTC
 AGCCTGGCGGACGCGGAA AAAAATCTTCAAGAAAGATACAAGGCCACTATGTCCGAGTCTCGCTCAACTCG
 CTCAGTGGCCATCGAGTGGACGCGAGGCTTACCACTAGGCTGGGTGATGCGGCCAGCGCCGAACTCTCA
 CCAAGCGGCACTGGCAGGGGCCCCGAGGACCAAGATGACAAGGATGTTGGGACTTCACTGGGACTGTGAGGC
 CTTCCCGACTACTCAGCGCCGACCCCATTAAGTGAACATCGGTGCTACATCTCAGAGACGACAGATCCA
 GTGTGACTGGACCTGTACAAGTCCCTCGAGGCTGGAAGACCAAGCTGCACATCGACACAGATGTGAAA
 CCGTCAGAAACAAAATTAAGAACTGTAGGGAAGTCCGAGGTCACCTGAAGAAAAGCGGCCAGAAATGTGAC
 GTGTCAAAAATCAGCTACCAACCCGACACAAAGGCCGCTCAGGACAGAGGCTCGAGTCTGCATCTTCTCAG
 GAGGGCTGCAAGAGAGGACAGGTGTGGCTTTCGGGAGCAGAGCGCAAGAAAGACTCCCAAGCTCG
 TCAAGCGCTGTGCAAGAACACGACAGCTGAGCATGCGAGGCTCAGCTGCTTCAACCAACAGCAGTACAG
 CAGACGGCGCTTCTGGACATCTGGGGCTTCTGTGCTGCACACGCGCAACATACAGCTACTGGTGCAT
 GAGGACCATCAATGAGCTCACAAATTCCTCTCTGTGAATTTGCAACTGGCTCTCTAGATGACTTTGATCTCA
 ACACAGACCCCTACCGACTGATGAATGAGTGAACACCTGGACAGGATGTCTCAACAGCTACAGTACAG
 CTCATGTGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAAACCCCGGACTCGAAACATGAGCTGATGAGG
 AAGCTTGTGACAAATACAGCGATTTAGCGTCAAAAGTGGCCAGAAATGAAGAGACCTTTCTTCAAACTCATGG
 GACAACTGTGGGAAGGCTGGGAAGGTGAAGAAACACACAGAGTGGACTCCAAAAACATAGAGGCATCACTGA
 TCTCAAGGCAATGA AAAACCTGTGGGTGATTTCCAGACAGCTGTGCTATTTGGCGAGGAGGCTGAGAAAGC
 AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACGAGGAGGACGAGATACCTTCAAGAACTCC
 ATTTTTCGCCCTGCTTTTGGCTTTGATTTATACCTCACCAGCTGACCAAAATGCAATTTTTCGATCAACAAAGT
 ACCACTAACCTCCCCAGAAGCTCACAAAGGAAAACGAGAGAGCGAGCGAGAGAGATTCTTGGAAATTTTC
 TCCCAAGGGGAAAGTGTGAAATTTTAAATCATAGGGAAAAGCAGTCTGTCTTAAATCCTCTATTCTT
 TGGTTTGTGTCACAAAGAGGAATTAAGAGCAGGACAGAGGCAACGCTGGAGAGGCTGAAAACAGCTCAGAGACG
 TTTGCAATGAGTCACTAGCAAAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCTCTGAAGAAA
 CTGCTTCAATGTATATATGTGACTATTACATGTAATCAACATGGGAACCTTTAGGGGAGACCTATAAGAAAT
 CCAAATTTTCAGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGA AAAAGAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHES
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHWMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQRVKDL CQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLDAAQ
PRNLTKRHWP GapedQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKD KVVLLREQKRKKLRLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTTLG
PFCACTSANNNTYWCMRTINETHNFLFCEFATGFLEYFDLNDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPPSSKSLGQLWEGWEG

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AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCCTCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTCTGCTGCTGCTGCTGCTGCTGGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCGGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
 ATCACCGTCATCTGGCCAGGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
 CCCCGCCACACCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
 CGCTCGCTTGAGGGTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCACAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTGCATGGCATGCCCCAGTGTACTATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
 ACAAGCGTGTCTTGGCAGAGCCAGCACCAAGTGGATGTGAAGTCCCGCTCTTGACCTCCTC
 ATCAGGCTGCTGCAGGCCTGTGGCGGCAGGGCAGCTGGGAGAGCCCTGAGAAGTGCCTTTT
 GGTTTGGAGAGGCAAGTGTGAGGCTGCACAGTCAATTCTACGGTGCCCTTAGTCCAAGAAAT
 AAAAAACCATAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAATGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGAGGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCC
ATGGCCTGCACCTCTCTGCAGTGCAGTTGCTGAGGAAGTGAAGAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCTTCTCTGCGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC
TCCAGGCCCTTGTCTAAGCCTTCTCCTCACTGCCCTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTTCTGCACCAAGCCCCAGGGCTGCCGCCCTGTTGTGCTTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAA
AAAAA

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FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATTRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTCTGGTGCCCCGGCTCCCT
 GCCCCGCGCCAGTC**ATG**ACCCTGCGCCCTCACTCTCCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCTCATTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAAT**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAA

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FIGURE 53

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNSKKK

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FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGAGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATGACACCTCCCTGA
CCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGCTGGTAGGG
ATGGCCATGGTGCCACCTCCTGGGCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAAATAAATTTAAAAAACTTAAAA

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CTGCTGCATCCGGGTGTCCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGAG
TGAGGCGGGCGGGCGCGGCACACCGGCTCCGAACCACTGCACGACGGGGCTGGACTG
ACCTGAAAAAAAATGTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTATTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTTATAGCAACCATAGCCTTCTTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTGCTCGCATTTGCGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGATTTTTTCCAGAATGCCTTCATCTTT
TTTTGAGGCGCTGGTTTTAAGTTTTGGCCGCACTGAAGACTATTGGCAGTGAACACATCTGAT
TCTCCACAGGCACAAAGCCCTGCATGGGTTTGTTTGTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAAATCTATTGTGGTATGCACCTTGATTAACCT
ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTATCATGGTATAATT
TGTAATAATAAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTGCTATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTATTCAAATGTGGT
CTCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAAAATATCCGTGG
TCAAAATCTCTCTCACTATAATTGGTATTTACTTTTACCAAAAAATCTGTGAACATGTAAT
GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGCTCTCCGCTGTGCCCTCATTC
CCAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATAACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGCGCGG
CGNGACACCGGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCGCTGGTGTCTCTCGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAGATTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCCTTCTCCGGAAGATGTC
AAACGGCCCCCAGCGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAAGC
TTTTTACGCCAACCAGTCCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCAGTCCCTGGTGTGGAACAACAT
ACCAGGCGAGGGGGCTGCTGTCAATCTTTGGAAAGAATGGCCCTTGAATTTGACACAGGAAT
CCATTACGTTGGGCTATGGAAGAGGCGAGCATTTGCCGTTTATCTTGGACAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCTGTCTCTCTCTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGGATACCCCATGTACAGTGGAGAGAAACCTTACATTTCAGGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCCGTGGTTACAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTCTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGCAGCAGCTGGGGGCCCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTACCGTGTCAACCCCAACCAAGTGCCTTTTCATGCACGCCCTGCTGGTCAACCATAC
ATGAAAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTTGCCCTTCCACACCATCCCTGT
GATTTCAGGGGCTGGGGGGCGCTGTCTCACAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTCACTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCCATCTGTGGTCTCAACAGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAAGCC
CCGCTCGCTGCCAGGTGTGAAGCAGCACTGGGGACGGTGGCGCCGGCTTAGGCATACCTT
CTGTCTTTCATCTGCCTGCGAGGCACCAAGGAAGACTGCATCTGCCCTGCCACCATCTACTAT
GTTTACTATGACACGGCATGGACAGGCGATGGAGCGTCACTGTCTCCATCCCCAGGGAAGA
GGCTGCGGAACACCATCCCTCTTCTCTTCTGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACGATTCCACGGCCGGTCCACCATGATCATGCTCATACCCACTGGCTACGATGGTGT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCAGTACCTATGAGACCTTCAAAAACCT
CTTGTGTGAAGCTCATATGTCACTGGTCTGAAACCTGTTCCCAAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCACCACTGTTCTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGCTGACCATGACCTGGGGCGCTGCACCTTGTGTGATGGCCCTCCTTGAAGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGACTGGTGG
GGGCGCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAA**TAG**TTCCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGCACGTATAAAGCACTCTAATTTGGTTCTGATGCCCTGAAGAGAGGGCTAG
TTTAAATCACAATTCGGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGTATG
TCTCATGACGCGGGCTCTGCATCCCTCACCCATGCCCTCTAAGTCACTGATCAAAAGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGTCAGCTCAACCTGGTGGGTTCAGTTC
TGCTCTGAGGCTCTGCTCTCATTTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAGGGAGACTAATGAGGCTTAACCAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTGGAGAGCTGTAGTCTCTTTTGTGCTGGGTTCACTGGAAGTCCCGGGTCTGTCTTCTTATCA
GCCTGTGTCTGGCCAGTGTGGTCTTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCTGTGAGATCATATCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCA
TCGGGGTGGCAGCTGGTCTCAATGTGCCAGCAGGGAAGTCACTGACTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGTTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCA
TGGATGGTGAAGATGAATCACTTTGCTGGGCTGAAGCAGGCTGCAGGCAATTCAGGCCAAGGG
CACAGCAGGGGACGTGTGAGGGAGGTGTGGGTAAGGGAGGGGAAGTCACATCAGAAAGGGGA
AAGCCACGGAAATGTGTGAAGCCCAAGGAATGGCAATTTGCAGTTAATTAGCACATGTGAGGG
TTAGACAGTGTGATGATCAAGCTCAAGGTTTGGAAATGCACTTTGAGTTATGTCTTTG
GTATCAGACATACGAAGGCTCTTTGTAGTTCGTGTTAATGTAACATTAATAATTTATTG
ATTCCATTGCTTTAAAAA

MWLPVLVLLAVLLAVLLCKVYLGLFSGSSPNPFSEDKVRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGLAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIDKYIKLVKVSSGAPHAILLKFLPLPVVQLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFMSHALLVNHMYKGGFYPRGSSIEAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELNIYCPIVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGMGTSVFICLRGTKEDLHLPSTNYYVYDMDQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLPQLEGGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGODIFTGCLVGALOGALLCSSAILKRNLYSDLKNLDSRIRAOKKKN

FIGURE 65

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA
 GGGGTTGGCACCGGCCCGGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG
 TCGGTTGCTGCTGAGCTTTGGCCTCGGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA
 AGAGGAAGACAGCCTCAAGAGCCAAAGAGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAAACCAGCTTTG
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGGCTGCTAAGAGA
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTCTATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC
 TCTTGGCTTTCTGTATGCCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGAT
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCCATGTTTGGTAAGTAGACTT
TAGTGGAAGGCTAATAATATTAACATCAGAAGAATTGTGGTTTATAGCGCCACAACTTT
 TCAGCTTTCATGATCCAGATTTGCTTGTATTAAGACCAAAATATTCAGTTGAACTTCCTTCAA
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA
 ATTTTCTTTAAATGATTAGTTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGC
 TCTTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTACATTAGATTATCATAA
 TTTTAAAAATTTTCTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC
 CCATTATTCTGGTCAATTATTGCTAGTGACACTGTGCCTGCTCCAGTAGTCTCATTTTCC
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACATCATTTTAAATAA
 ATTATGTCTAAGATTAATAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPNKDYEPPKVRKPALTAIEGTAHG
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEAAKRRQMGEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMF EK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCTTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGGCCACAATGCCT
GTGTCTTACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

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FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQGVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

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FIGURE 69

GCGCGCCCGCCCGAGACCGGGCCCGGGGCGCGGGCGCGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGGCACGCCGCGGGGCCCGGCCCTGACCCCGCGCCCGCCCGCTGAGCCCC
 CCGCGCGAGGTCCGGACAGGCCGAGATGACGCGCGAGCCCTGTTGCTGCTCTGCTGCCGCG
 CGCTGCTGCTGGGGGCTTCCACCGCGCGCGCGCCGAGGCGCCCCAAGATGGCGGAC
 AAGTGTGCTCCACGGCAGGTGGCCGGCTGGCGCGCACTGTGGCGCTGCAGTGGCCAGTGGGA
 GGGGACCGCCCGCCGCTGACCATTGGGACCAAGGATGGCCGCACTCCACACGCGGCTGGA
 CGCGCTTCCGCTGCTGCCGAGGGGCTGAAGTGAAGAGGTGGAGCGGGAGGATGCCGGC
 GTGTACGTGTGCAAGGCCACCAAGGCTTCGGCAGCCTGAGCGTCACTACACCCTCGTCTGT
 GCTGGATGACATTAGCCACAGGAAGGAGAGCCTGGGCGCCGACAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTACACAGCCCTCCAAAGATGAGCGCG
 CGGGTGTATCGCACGCGCCGTGGGTAGCTCCGTGCGGCTCAAGTGGCGTGGCCAGCGGGCACCC
 TCGGCGCCGACATCACGTGGATGAAGGACGACAGGCTTGACGCGCCAGAGGCGGCTGAGC
 CCAGGAAGAAGAAGTGGACACTGAGCCCTGAAGAAGCTGCGCGCGGAGGACAGCGGCAATAC
 ACCTGCCCGGTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGTGGATGTGATCCA
 GCGGACCCGTTCCAAGCCGTGCTCACAGCACGCCCGCTGAACACGACGGTGGACTTCG
 GGGGACCACTGCTTCCAGTGAAGGTGGCGAGCGAGCTGAAGCCGCTGATCCAGTGGCTG
 AAGCGCTGGAGTACGGCGCGGAGGGCCGCACTCCACCATCGATGTGGGCGGCCAGAA
 GTTGTGTGGTGTGCCACGGGTGACGTGTGGTGGCGGCCGACGGCTCCTACTCAATAAGC
 TGCTCATCACCGGTGCCCGCGAGGACGATGGGCGCATGTACATTGCTTGGCGCCAAACCC
 ATGGGCTACAGCTTCCGCGAGCGCTTCCCTACCGTGTGCTGCCAGACCCAAAACCGCGAGGGCC
 ACCTGTGGCGTCTCTGCTTCTCGGCACTAGCCTGGCTGGCCGCTGGTGTGCATCCGGATCCGAG
 CCGGCGCTGTCTTCATGCTGGGACCCCTGCTCTGTGGCTTTGCCAGGCGCCAGAAGAAGCCG
 TGCACCCCGCGGCTGCCCTTCCCTGCTGGGACCGCGCGCGGAGCGGCGGCGGACCG
 CAGCGGAGACAGGACCTTCCCTGCTGGCGGCCCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGATGGGTCTCCGCGAGCCCCCAGCACTTACTGGGCGCGCCAGTGTGCTGGC
 CCTAAGTTTATCCCAAACCTTACACAGACATCCACACACACACACACACTTCCACAC
 ACACTTACACGCTGGAGGCAAGGTCCACCAGCACATCCACTTCACTAGTGTAGACGGCACCGT
 ATCTGCAGTGGGACCGGGGGGGCGGCCAGACAGGAGAGCTGGGAGGATGGAGAGCGGAGCT
 GCAGACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGACACCCAGGCGAGTGTGTGT
 TGAGCATAGCCCTTGACACACACACACAGACACACACTACTGGATGCATGTATGCAC
 ACACATGGCGCGCACAGTGTCTCCCTGAAGGCACACGTACGCACACGCATGACGAGATATG
 CGCGCTGGGACACAGATAAGCTGCCAAATGCACGCACACGCGACAGAGACATGCCAGAACA
 TCAAGGACATGCTGCTTGAACATACACACGACACCCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACCGGATATGCTGTCTGGACGACACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTTGACACACACATGCACGG
 ATATTGCTTGGACACACACACACACACGCGTGCACAGATATGCTGTGTCGACACGCGCAC
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACAGGCGCAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTACACACACACGCGAGACATGCTGTCCGGACAC
 ACACGCGATGCACAGATATGCTGTCCGGACACACACGCGACAGATATGCTGCTGCTGGAC
 ACACACAGATATATGCTGCTCAACACTCACACACGTCAGATATGCTTGGACACACACA
 TGTGCACAGATATGCTGTGGACATGCACACACGTCAGATATGCTGTCCGGATACACACG
 CACGACACATGAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACACAGGT
 GCAGATATGCTGCTGGACACACACAGATATGCTGCTCAACACTCACACACGTCAGATATG
 TATTGCTTGGACACACACATGTCACAGATATGCTGTGTCGACATGCACACAGTGCAGATA
 TGCTGTCCGATATGCACGCGACACATGCAGATATGCTGCTGGGACACACTTCCGGACA
 CACACATGCACACAGGTGCAGATATGCTGCTGGACACACGAGACATGAGTGTCTTTGG
 GAGGTGTGCCGTGACGCTGAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGAGACTTT
 CCTCTGCTCACCGCTCACTCCCCAACTTGTGCCCGCTCTGTCCCCGCTCAGTCCCCGCTC
 CATCCCCGCTGTGTCCCTTGGCGCTATTTTGGCCACTTCTTGGTGTGGTGGCGCCAG
 AGTCCCCCTACTGTGTGGGCTGGGGTGGGGGACAGCAGCCCCAAGCTGTGAGAGGCTGGAG
 CCGATGGCTATGGCTCATCCCCAGTGCATTCTCCCCGTGACACAGAGAAGGGGCTTGTA
 TTTATATTTAAGAAATGAAGATAATTAATATGATGGAAGGAGACTGGGTGTGAGGAGAC
 TGTGGTCTCTCTGGGGCCCGGGACCCGCTGCTTTCAGCCATGCTGATGACACACCCCG
 GTCCAGGCGACACACCCCGCCCGCCACTGTGCTGGTGGCGCCAGATCTCTGTAATTTTA
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAA

FIGURE 70

MTPSPLLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFGGTTSFQCKVRS DVKPV IQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

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FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTCA
 AGTGACTCTGTGAAGACCCACATCTACCTTCTTGCCACGTTCCACCGGGCTTGGGGGAAAGATGGTGGGGACCA
 AGGCCCTGGGTGTTCTCTCTCTGCTTGGGAAGTCACATCTGTGTTGGGGAGACACAGCATGCTCAGGACTCA
 GTAAGAAGAGTCCAGCTGGGAAGAAGAACCCACGATCTTTTGCCAAAGCCTTGCCGACACCCCTGGAGAGCCCTGG
 TGAGTGGACCAACTGGTTTCAACATCCGACTACCCAGGCGGGAAGGGCGCACTATGAGCGGCTGGACGCCATTGGT
 TCTATATGGGACCTGTATGTGCTCCCTCGCGCTTGAGGGCTCGGACCTGACTGACGACCTGAGCAGCTGGGCG
 AGCACTGGCCAGAGCTGTCATGGTAGTCCCCGTGAGGGGTTTCTGGTGCCTCAACAGGGAGCAGCGGCTGGCCCA
 GAACTCGCTTAATTACACGCTGACCTTCTCTGCCCCACGAGGTCCCTGGCCGACGACACAGCGCATCTGGA
 GCCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCCCTGTGGTCAGACTGGGGTCCAGACTCGCACACCGCATTTGCT
 TTGGCAGAGATGGTGTCCGCTGTGCACTGAGGCCAGCAGAGGGGTGAGCATGCACTGGCCGAGGACTGTACAGC
 CTGTGACCTGACCTGCCCAATGGGCGAGGTGAATGCTGACTGTGATGCCCTGCATGTGCCAGGACTCTCATGCTTC
 ATGGGCTGTCTCCCTGCTCCGAGGATGTCGCCAGCTCAGAGGGCTGCTATCTACCTCTGACACAGGCGCGAG
 CTGCTGACCCAGACAGACATGGTGGGAGATTCGGAATCCCTGGCTTGTGGCCTGATGCGCAAAAGCATCTGAA
 GATCAAAAGGTCAAGTTTGCCCCCATTTGTACTCAATGCCAAAGACTAGCCTGAAGGCAGCCACCATCAAGG
 CAGAGTTTGTGAGGCGAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCAGGAGCTGGGCAGAGC
 GTGTCTCTGTGCTGTAAAGGCCACAGGGAAGCCAGGCCAGACAAATATTTTGGTATCATAAATGACACATTTGCT
 GGATCTCTCTCTCTACAGACTGAGAGCAAGCTGGTGTGAGGAACTGCAAGCAGCAGCCAGGCTGGGGAGTACT
 TTTGCAAGGCCAGAGTGATGCTGGGCTGTGAATTCAGAGTTGCCAGCTGATTTCTCAGACATCTGATGAG
 ACTCTTTCGAACCCAGTTTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAGAAATGCCAACCTGCT
 CCTTCTACTATGACTGGGGACCTGCCCTGTTAAGACTTGTGACGGGCAGCAGGATAATGGGATGAGCCGCTG
 ATGCTGTGCAAGACTGCTGTGGCATCTCCAAGACAGGAAAGGGAGATCCAGTGCAGTGGCTACACGCTATCCC
 ACCAAGGTGGCCAAAGAGTGTGACGTGCCAGCGGTGTACGGAAACTCGGAGCATCTGTGCGGGGCGGTGTGAGTC
 TGCTGACATGGGAGGCCCATGCGCTTGGCCATGTGTACATGGGGAACAGCGCTGTAGACATGACTGGCTACA
 AGGCGCATTTCACTCTCATGTCCGCGCAGGACACTGAGAGGCTGCTGTCTCAATTTTGGACAGCTGTGAGAG
 TTTGTCAACCCACCAAAAGTGTCTACCTTTCAACAAGAGGGGAGTGGCGTGGTCCATGAATCAAGATGCTTGG
 TCGGAAGAGGCCATCACTTTGGAGGCCATGGAGACCAAGCATCATCCCCCTGGGGGAAGTGGTGGTGAAGACC
 CCATGGCTGACATGGAGATTCTCCAGGAGTTTCTACAGGCAGAAATGGGAGCCCTACATAGGAAAAGTGAAG
 GCGAGTGTGACCTTCTGGATCCCCGGAATATTTCCACAGCCACAGCTGCCAGACTGACCTGAACCTTCATCAA
 TGACGAGGAGACATCTTCCCTTTCGGACGATGGCATGTCTCTGTGCTATGACAGATGAGGTCACCTCAG
 AGCCACTTAATGCTTGGCAAGAGTGAAGTCACTGTCACTGAGAGTCAAGATCGCAGAGCATATATCCCA
 GTGAACTCTGCTCACTCAATCCAGACACAGGCTGTGGGAGGAGGAAGGTGTTCAAATTTGAAATCAAG
 GAGGAACAAAAGAGGAGACAGAGACTTCTCTGGTGGGCAACTGGAGATTCGTGAGAGGAGGCTCTTAACTCGG
 ATGGTCTCTGAAGAGCGGCGGCTGTTTGAAGCTGAGGCGCTACCGGAGTGAGAGGTTCTTGCTCTGTAGGCAG
 ATCCAGGGGGTGTGATCTCCGTGATTAAGCTGGAGCTAGACTGGCTTCTGTGCACACCTAGGGCTGGGG
 CCGCTTTGACAGTGTATCAGAGGCCCAACGGGGCTGTGGTGGCTTGTGACAGGAGTGTGCTGATGAGT
 CTCTACTTGGCTTATGCTTGGCAAGCTTGGCTGGGGAGGAAGTCAAGAGCTGGAGTGTCTCTCAAATTAAC
 CCAATGCAATTTGGCGTCCCTCAGCCCTATCAACAAGCTCAACTAGCCTGGACGAGGACATGAGGATCCAG
 GGTTAATAAAGACAGCTTTCAGATTAGCATGGCCAAGCCAAGGCCAAGTCAAGTCAAGTGAAGAGAGCAATGGGCCCA
 TCTATGCCCTTGAAGAAGCTCCGGGCAATGTGAAGAGGCCACCCAGTGCAGGCCACTTCCGGTGTCTACAGAT
 GAGGGGGATTCGATATGACTACACACAGTCCCCCTCAACAGAGATGACCTATGAGCTGGATCGACAGCATATCT
 GGCATGGTGGCCAAAGCCGATGATTCAGGCGCTATATCAAGCTGAGTTTGGGGCCACTGGAAGTGA
 ATGTGCGATTCGCCCAACTGGGGGCACTCATCGCGGACAGTGGGGAAGTATGTGAATCCGAGATGTGAGG
 AGCACTCGGGACGGGACAGGCCCAATGTCTCAGCTGCCTGTCTGGAGTTCAAGTGCAGTGGGATGCTCTATGA
 TCAAGGACGCTGTGGACCGCACCTGGTGAAGGTCACTCCCCAGGGCGAGTCCGCTCGAGCCATGCTGTGAACCCCA
 TGCTGATGAGTACCTGGTCAACCACTTGCACCTTGCAGTCAACACGACACCAAGTGAAGTACACCATCTGTGGCA
 CCTTGGACCTGCTTTTCTGATATGCTGCTTCTGCTTCAAGCTGTGACGAGGACTCTCGCACAGGAGTCTTGT
 CGCCTTGGCGCGGTGCTTGGCGGCACTCCGATGGCTTCCCAAGATCTGAAGAGCAATGTGGGATAGGCC
 TCACCTTCAACTGTGTAGAGGCGCAAGTAGGCCGCGAGGTGCTTCCAGTCTCCAAAGCACCCCGACCCAG
 TCCCCGTGTCAGGAGCTGTCAAGGAAGATGCGCTCGAGGAGGACGAGCAGGAGGAGCGGGGTGGCCACGG
 CCGGGTGAGTGGTGGCTCTCTGAGATTCTAGAGTTCTCAACAGGCCCTGATCAATTAAGTGTGGT
 ACTTACCTCTTCTGCCCTCATTTGATGTGACGCCATTTGAGACTGTGACCAAACTGCTACCTTGGTAT
 TTAAGCACTCTGTTTCTGATATGCTGTTCTTCTTCAAGCTTCTTCAAGCTTCTTGTCCCTTCTATCA
 TTTGGCACTGGCCCAAGCCCAATGGCACAATAAAGCCCTTTGTGAACATGTTCTTTAAATGAACACAGAATAAT
 TGGCCATGTTAAACTTCTGACGTTTCAACTGTACTTCAATTAATGCCATTCTTCAAAATATCTCTCTTCT
 TTGTCATGGTTTGGCCCACTCTGCAATAGTGATATCTGATGCTGAAGATCAAAATAACCAATTAAGCATAT
 TTTCTGGCCTTGTCTCCACAGGACATAGGCAAGCCTTGAATCATAGTTCAATACATAAATGGTGGTGAATAAAG
 AATAAAGACCAATATCTTACTTGAATGTAATTAATCTATTTATTTCTTGCATAAATTTGGAAATCTAGTGC
 ACTATCAAGCTTAAGCTATTAATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 ATCCAATTAACACAGGTTGCTAAGTATTTGTATCTTCCCTTGCATTCGCTTTGTCTCTGTCAGAAAC
 CCAAGTGTAGCCGAGGCGAGATGCAATAATGCATCTCTGTATTTCGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGS PREGFWCLNREQ
 RPGQNCNNTYRFLCPGSLRRDTERIWS PWS PWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDSGRFRIPGLCPDGKSLKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQONATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCKGISKTEEREIQCSGYTLPTKVAKESCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNNTKVLFPN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPIYIGKV
 KASVTFLDPNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVYRYSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNIAIGVPQPYLNKLNRYRRTDHEDPR
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPFPN
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVI PQGSCRASVNFMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

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 10611 266860 F

FIGURE 73

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTGGGATCTGCTTGGAGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTTATATATGTAACATAGACAAAAGATCCGAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAGATTACAAGAATTTAGAGATGATTTGTCGAAGTCCCTGCTGATTCACTG
 CCCTTTGGGTTTACGCTGTCCTCACTGATGCAGCCTACCCCTTGGTTGGGGACATTATGATTTGCTAAGACT
 CAGATTTACACGGAAGAAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGACATGACAAAATA
 TCTGAAGTGAARCTCGATCTCTCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGCGCAATC
 CTTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGAGTATCCCAAGCCTCTCCAGGTTAACT
 CACTCTGTCTTGGAGCAAAACCATTTAGCTAACAGACAAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCOGTGAAGGATTATCACAGCATACGGTCTTAGAAATCATTTGCACAGA
 AGAGTACTCAACAGGGTATACAAACAAATAGCAAAATTAATCCACTTTGAATCAAGACAGGTTCCGCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGAAGCTGGATACACCAAGAAACTCAGAGATTCTTT
 ACAGTACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGGATCTCAGACATAAAGGTGCGAGGAAGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAAACAGCAAATTCAGATGCGAATGTGAGCACAACTACAGTCCAGACTCTGGGAAATGCAAGAAG
 AATTTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGACGAGGAGCTGCCACA
 ACAACGTGCGCTGCTGTGCCCCGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCAGCGCTGCTGCTGCTGACCACGCTGCT
 GGGAACCGCCAGCCCCCTGGTGTCTAGGTGTCACTCCAGCCACACCCGACGGGCTGTGCGGTGGGGGAAGCA
 GACACAAACCAACATTTGCTACTAATACATAGGAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 TGAAGAAGGCCTAATGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTCT
 TGACTCCAGAGGAGTTGGCAGCTGTGATATTTATCACTGCAAAATCAGATTGGCCAGTGCAGAGCATATTTGGA
 TTGGAAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAAACAAATCAACCGAACCCTAAAAACATTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGGACCAACAAATAGCATTCTTTGGTGTGACG
 GTGCTTTTGGGCATAAGGAATCTGTTACAAGCTGCCAATTTGGCTGCTCCGCTCCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAACCCCTCGTTGGTTGAAGATTCTTTGCTGATGTTAGTATGACACA
 TCTGTAAACGCCCCCTCAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGACTGAGTCCAGTGGCA
 GCACACACCCACTATACAAGACTGGCTATAGGAAAAAGAAAGTGTATCTATCCTTTGATATCAATGAAGTT
 ATTTTCTTGAACACTGAAATATGTAGATTTTGTATTAATTTGCCAATTTGTGTACACACAATCTGTTAAT
 GTATCAATTCGAATCGAAAGACTGACATTTATTTTGTCTCTTTCGTTCTGTTTTCCTGCTGCAGA
 GATTTCTCTGTAAGGCGAACGAGCTGCTGGCATCAAGAAATATCAGTTTACATATATAACAGTGTAAAGA
 TTCACCAAAAGGACATTCTAAATGTTTTCTTTGCTTTAACACTGGAAAGTTTAAAGAAATAAAACCTCTGCA
 TAAACGATTTTCAGGAATTTGTATTGCAATTTCTTAAGATGAAAGGAACGCCCAAGCAGTTTTCACACTCACT
 TTAGCTGTTCTGTGTGGACTGAGTACATTACGCTGACGAATTTAGTTCCCGAAGAGATGAGTTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCACCTTGGGAAAAATTACACAGCAAAAAA
 AAAAAA

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FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLTTLLGTAS
PLVF

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CCACACGCTGCGGGTGACCTGGGCCGAGCCCTCCCGTTCGGCTAAGATTGCTGAGGAGCGCG
CGGGTAGCTGGCAGGCCGCCGACTTCCGAAGGCCGCCGCTCCGGGCGAGGTGTCTCATGACTT
CTCTGTGTGACC**ATG**TCCGTGATCTTTTTTGCTGCGTGGTACGGTAAGGGATGGACTGCC
CCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
AGAGTTTAGCCTTGCAGCTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
AGTATACATTTTTCTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
AGCAGCCATGGCCTTCTGCTTCTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA
CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAG
AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAAT
TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGACACAGAATGTGGCAA
ATGGGGTGATGAATGGTACACACCGATGCACCTTGGAGCCTGCTCCTAATTTCGGAATGGAA
CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCTAACATCATGTGTGCTGCCCTGAATCT
CATTTCGAGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
TGGACCAAACTCTG**TGA**CCAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
CCGGGAGCAGTGATGTCAAATTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
AAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
ATGTCAGAGCTGTTGCCACAAAGCGCCTTTTATTAGGGTAAAAATTAACAAATCCATTCTAT
TCCTCTGACCCATGCTTAGTACATATGACCTTTAAACCTTACATTATATGATTCTGGGGTT
GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCCAGGATTCTATTTTGT
TTAATGGGCTTTTCTACTAAAGCATAAAATACTGAGGCTGATTAGTCAGGGCAAAACCAT
TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTCT
TTGTAACAATAAATATTTTGGAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
TAAACTGTATATAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
AAGTGGCTTCGAAATGGCAGAATAAATCTAAAGTGTTTATTTAAAAAAAAAAAAAAAAAAAAAA
AAAAAG

FIGURE 76

MSVIFACVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFQDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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TGCTTCCTGGAGACCTGTGGTGGGAATTCAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAAGTGAAGTGGCATT
 TTAACATATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTAAACAGAGGCGGGTGGT
 CCTGCCCCCTTAAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTTCGAGGGTGGCAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGGCGGCGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
AGGAGCACCCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCGTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCAACACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCAACCTGTCCCTCA
 TCTTCTCATGCCCCTTGCATATTCTTCACTGAGTCTGAGGGCTTGTCTGGCTCCAGAAAG
 GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACC CGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
 CTACACAGACAGGTCTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCTGGCAACGGAACTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGTCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCGTCACTTACGGTTGTAATCTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCTGCGGCCAGATGGCAGCACACTGCCATGACGCAGATAATT
 GGGAACTGTGCTGTCTCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGG
 GCTCACTCGCTTTGACCTGTGCGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCAGCCTTTGCAAGGCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGCGAGAGCTGATCCGGGCTTTGGCTGGACAGACTGCCGCTGCCCTC
 CTCGGTTTCCCCCAGGCATCTAGGAAGACCAGCACCAGTGAACCTCCAGCTGGGGTGGGA
 AGGAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTTGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACACATCA
 ATCTGCCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGGTAGGGGAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCTCTGGCCACGCAAGCCTAAGCACTGTGCTATCTGAGGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

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FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFVSTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLI FYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTICLVKTFTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

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FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAGG**CCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

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FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTGTCTGTATACCTCATCGGGCGGTGATTGCCGACGAGATTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCAGGAGAAATCCAGGATCTGGGTG
 CTGCTTATGAGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTTCACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCAACAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAAGTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCATTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTTGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTA

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FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFDLGAAYEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGMFGGTPRQQ
DRNIPRGSDIIIVDLEVITLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVDCDECPNVKLVNEERTLEVEIEPGVRDGMIEYFFIGEGEPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

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FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTINTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAGGAG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG
GAGAAATTCCAGGATTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

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FIGURE 87

GGCACGAGGCGGCGGGCAGTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGCC
 TTGGTGCTGGTTTGACGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCTGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTGACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCTCCGTTGGACCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCTGAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGTGAGGAGCATTGGAACTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCTCTGCAGGAGCAGTCTGCAATT**TAG**TGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCGTCAGTTTATGCCTCTTTTGAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTGTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAACT
 ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACCTTATGTTTCCCTCAAAAAAAAAAAAAA

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FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIALKICHTLTEKLVAMTMGSGAKMKSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTCTTCCGACTCAGCTTCCACCCTGGGCTTTCGAGGTGCTTTCGCCGTGTCC
CCACCACCTGCAGCCATGATCTCCTTAAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTTTTGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGAAAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATTGGTTTAGAAAGAACATTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
GGGCTTCTTCTGTGCTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
AGTGAAATTGAAGACTCATTTAAATATTGTGTTATTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCTGTTTCTTTCTTTTATTTGAAAGGCTCAGGAGCATCCATAGGCATTGTCT
TTTAGAAGTGTCCACATGCAATTGGCCAAAATATTTCCAGTTGCATGTATCTCGAAGATGA
TGCATGAATTTCGATTGGATTGTGTCATTTAAAGTATTAAAACCAAGGAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTNGNCNCAGGGCC

FIGURE 90

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLEFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRRVPLGSLNLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

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FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTCCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGACAGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCTCGATCTTTCTTCTCTGGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCGTGTGCCACCTGGTCTTCTGTACGTCTTTATTGCTCAGGGCTAATC
 ATCAACACCATTACAGTCTTCACTCTCTCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGTCTTGCCCAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTTCT
 GATTCACGTGTAGGGCACACGGTTCACGGAGAAGAGCATGAGATCAGCATGCAGTGGCCC
 GGGCCAAGGGGCTGCCTCGCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGTCTGTATGACTGTACACTCAATTTAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTTACGAGGAGTACTACAGGACGGGCACCTTCCGAGA
 GACGCCCATGGTGCCCCCGCGGCCCTGGACCTCGTGAAGTGGCTGTTTTGGGCGCTCGC
 TGGTGCTTACCTTTCTTCCAGTTCTGGTCAAGTATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTATCTCTGCTCTTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAAGTGAACCTTTGTTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGACCGAAGGGGACAAGTTCCCTTTTCACTCTTGGTGCTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAGAGTCTTTAGGTGAGATGACTAAATATGCCTC
 CAAGAAAAAAATTAAGTGTCTTTCTGGGTCAAAAAA

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FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDS
KQKLND

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CTGAGCGCGCGGTAGC**ATG**AGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
CGGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
GTAAAAGGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTA
TACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAG
GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAAATGTGGTAGGT
TGGTACAAATTCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
AAACTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA
TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
TTTCACAGGGTACCTTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC
TGTATCAGGTTCCGTGATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAAATGAATGTATGCTTCATTA
CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAGCAGTAGATAAACT
AGTAAGAGTGTAACACAGATTAACACGAAATTTGAGAAAAGGAGAGGAGCAGAGATTGAGG
CAGCAAGAGAGATAAGCAATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTGACGGCATT
CGGACCTTTTTTCCAATTTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
TGTTTTCTAAAGTAGCTGTAACACACACCACCTCTCGATGTAGTAGACAATCTGACCTTAA
TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAATCATTAGCAT
AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC
CAGAAAAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAAATATTCAGGCTCCTACA
TTTT**TGAT**CCTTTTAACCTTACAAGGAGATTTTTTTATTGGCTGATGGGTAAAGCCAAACAT
TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTTTACTATGTTTAC
CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTTCACAAAGTACTTTTTCAAAC
ATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCCTAAAGTTGTTGAGGGGAAGGCT
TACACAGACACATCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACAGCC
TGGGCAACGATTTGAGACCATGTCTATTAATAAATAAAATGAGAAACAGAATAAGCTTTAT
TTTCAAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAAATTTCTCCTTAAG
TGATACCTTTTTTAGAAGTACATATATGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
ATAAATTTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTGFLLEGVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHLDVVDNLTLMEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCACAGCCGCGCGGGAGGCGAGAGTCAGCCGAGCCGAGTCCAGCCGAGCGAGCGGACAGCGCAGGCGACG
 CCAACAGCGCGCGCAGCGAAGCGCCGCGCGCCACACCCCTCTGCGGGTCCCGCGCGGCTTGCACACCCCTTCCCT
 CCTTCCCGCGCTCCCGCTTCCCTGGGCGCGCGCGCTTCCAGCCCTCTCTCTCCCTGGCGCGCGCTGGCACCG
 GCGCGCGCTTGCCTGAGCGAGGCGCAGCTCTACTTTTCCGCGCGGCTCTCTCTCCCTGCTCGCTCTTCCAC
 CAACTCCAACCTCCTTCTCCCTCCAGCTCCACTCGTAGTCCCGAGCTCCGCGAGCCCTGGCGCGCTGCGGAT
 CGCGCTTCCCGTCCGCTCCCAAGGTGGGAAGCGCTCCGCGCGCGCGCGCACCTAGGCGAGGTTCCGCTTCC
 CGCGCTTCTCTGCACCCCTGGCAGTGCTCAGCGCGCGCTGCTGGGTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTGGCAGCTCTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCGCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTGTTCAGTTACAAGAAAGTTTG
 ATGAATCTTCAAAGAACTACTTGAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTCTGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTAGCAAGTATACGGAGCAGCTGAAGCCCTTCGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTCGCTCAAGGCTTACGGTTGCGGG
 AGATGTCGTGAGCAAGGTTCTCCGTGGTAAACCCACAGCCAGTGTACCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCCTTTCAACATGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATAATAGTGTTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT
 TCTCGTCCATCTCTGAAGAGTGCTTCAAGTGTCTGCTTCAAGACACATCAACCAGGGAACGCCCAACACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTCGTCTC
 CCCTTCCGAGCAACGTTTGCAACGATGAGAGGATGGCTCAGGAAACGGCRATGAGGATGACTGTTGGAATGGG
 AAAGGCAAAAGCAGGTACTGTTGCGATGACAGGAAATGGATAGGCCAACAGGGCAACACCCAGAGGTCCA
 GGTGTGACACAGCAAAACGACACATCTGATCCTTCTGCAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCATCAATGGGAACGAGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAGAGGAGTGGAAAGT
 GGTGTGATATCAGCAGTGCCCTTCAAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGGCAATGA
 GAAAGCCGACAGTGTGGTCCGTCTGGGGCACAGGCCCTACCTCTCACTGTCTTCGATCTTGTTCCTGG
 TTATGCAGAGAGTGGAGATTAATTTCTCAAACTCTGAGAAAAGTGTTCATCAAAAGTTAAAGGCACAGTT
 ATCACTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACACCAATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGATGCTGACTTTGTTTCTCATTCACTTTGGGAGGAAAAGGACTGTGCATTGAGTTGGT
 TCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTCTGTTTGTGGTTTGTGGTTTCTTCTCAACTGTATCT
 CGCCTTGTCTTACAGCAAAACAGGTCCTTCTGGCAGTAACATGTACGTATTTCTGAAATATTAATA
 GCTGTACAGAGCAGGTTTATTTATCATGTTATCTTATTAAGAAAAAGGCCAAAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSSELFKDLFVELKRYVVGNNVLEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNFFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPNVCNDERMAAGNGNEDDCWNGKGSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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CTTCGCCCTCAAATGGGAACGTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAGTCTTAATCTCTTCCCTCCTCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCCAGAGGGCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTGATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCCCTGTGATCATTTCAGGGCAATGTGAAGAAAAAGACACCCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTGAGTAAGAAGCTT
TGCTCTGCCTTTGCTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTCTCCACCTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTGTGCTCTC
TCTAGTGTCTTCTCTCTCGTCACTTAGCCTGTGCCCTCCCTTACCAGGCTTAGGCTT
AATTACCTTGAAGATTCCAGGAACGTTAGTCTTCTAGCTAGTGTCAATTAACTTAAATGC
AATCAGGAAAGTAGCAACAGAAAGTCAATAAATATTTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLPLMLSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKNVKKTRHQRRHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATT CAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRRLTVVLGLLVLFILTCYADDKPKPDDKPDGKDPKPDFPKFLSLLGTEI IENAVE
FILRSMRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGCTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTCTGTGTCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCT
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCTTCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CGGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCATGCGT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT
 CTCCCCTACTACCCTTCTCTCTGAGCTGGGGGCACCAAGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAGAGGCAGAGGTTTTGTCTCAATATTTTTTAATAAATAGACGA
 AACCACG

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FIGURE 103

MDILVPLLQLLVLLLTLP LHL MALLGCWQPLCKSYFPYLM AVLTPKSNRK MESKKRELFSQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTCLDPNPHFEKFLT KSMAENRHLQYERFVV
APGEDMRQLADGSM DVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLP LRG T

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FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCATAACTTTTGAAGGAA
 AAGTAAAGGAGGATCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGTGAAAACCTGACGGAATGGAACGACAGAATATACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT
 GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCGCCACCTTGGTTCAGTGCTGGAACGATATTACCTCAGTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAATTC AACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAATTTGAACTGTAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTCTT
 ACTACAACTGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAAACCTGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRONITNQLEKWMKLNVEEGLYSRTLGSITTPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAALLHWNHGLKPGWRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCGTGGTTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

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FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGACAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGC GCGGGCGCTGAGCTGGCAGGCGGGTTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCTGCACTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCCTGTGGTCATCGTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCATAAATTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCACAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGCCGCCACCTTGGTTCCAGT
 GCTGGAAAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCA
 GACCCAACAGGCAAAATTAACCTAATCCGAAGATATACCGAGATCTCAACATATAAGTGAAA
 CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATCGCTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAACCTGCTGTTGGTTTTAATTTT
 GTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGTTAAAAA

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FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCCTGCCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCATGGGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTGCTGGGTTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCAG
GCTGGGCCCTCCCCCTGGTGCTCCAGTGTCTTGGTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAAAA

CGGCTTCTGGCT

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FIGURE 109

MGAATISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVETPALAPVLRPHH
PRSPAMKAATCCSPEGFWPSLEPRT

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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTAAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTGTCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTA
 TCCACAGGCATCAGGCAGTGTCTGCTCGTCTTGTATTTTGTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGTCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTATGGAAGCGGCCAAGTGAATATAAGCCCCCT
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTTCGCTGCCAGCAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAGTCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAACTGCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTGTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTTAAACAATGCAAGGGCAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGATAGATATCCCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCTTCTCTCAAAA

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FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFACTSAKDAFKIL
SKNSSHFTSINCFGDFII FLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT
 AGAATAATTGTATGGGATTTGTGATGCAAGGAAAGCCTAAGGGAAAAAGAAATATTCACTCTG
 TGTGGTGAAAATTTTGGAAAAAAATTTGCCCTTCTTCAAACAAGGGTGTCTATCTGATATT
TATGAGGACTGTTGTTCTCATTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTTGCTGG
 TGACTGCGAGTACATTCAAACAAAGAAACGGCAAGAAGATTAAAGGCCCAAGTTCACTGTG
 CCTCAGATCAACTCGGATGTCAAAGCCGGAAAGATCATCGATCCTGAGTTCAATGTGAAAAT
 TCCAGCAGGATGCCAAGCCCAAAATACCATGTTTATGGCACTGACGTTGATGCATCCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGAGGGGAAAATACTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT
 ATCCCTACACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTA
 CCTACCCATCAGCTTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGAC
 ACAAAAGCCTATCAGAGGCCACTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAGGCCATCCCTTCTG
 CTGCTTCTACCCAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTCAAGCTGGGAC
 TTGTTCCAAAAGAAGAAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 AATCCGAAGCAGCTCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCGCTCCAC
 TGATGGGTGTGTTCCAGTATGGAGACAACCTGCTACTCACTTTAACTCAAGACACACAG
 AATCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGACTTTCTAATGT
 AGGTCGGGCCATCTCCTTTGTGACCAGAATCTTTTCCAAAGCCAAATGGAACAGAAAGCG
 GGGCTCCCAATGTGGTGGTGGTGGTGGTGGCTGGCCACAGGACAAGTGGAGGAGGCT
 TCAAGACTTGGCAGAGAGTCAAGAAATCAACATTTCTTCACTACCAATTGAAGTGTGCTGA
 AATAGAGAAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAGGCCGTGTGCAGAACAAAGC
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCTTGCAGCCTCTGGTG
 AAGCGGGTCTCGACACTGACCGCTTGGCTTGCAGCAAGACCTGCTTGAATCGGCTGACAT
 TGGCTTCGTCTGACAGGCTCCAGCAGTGTGGGACGGGCACTTCCGACCGTCTCCCTCAGT
 TTGTGACCAACCTCAACAAAGAGTTTGAGATTTCCGACACGGACACGCCGATCGGGGCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCTGACAT
 CCTCAACGCCATCAAGAGGTTGGCTACTGGAGTGGTGGCAGCAGCAGCGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGTCTTCAAGAAGTCCAGGCCAACAAAGAGGAAGTTAATGATCCTC
 ATCAACGACGGGAGTCTACGACGAGCTCCGGATCCAGCCATGGCTGCCATCTGAAGGG
 AGTGATCACTATCGATAGAGCGGTTGCCCTGGGCTGCCCAAGAGGAGCTAGAAGTCAATGCCA
 CTCAACCCCGCAGAGACCTCTCTTTGTGGACGAGTTTGACAACCTCATCAGTATGTC
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTCAGAG
 CAGGCAGAGCACCGCAAGTGCTGCTTTACTAACTGACGTGTGGACCAACCCACCGCTTAA
 TGGGGCAGCCAGCGTGCACTCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTGTATTAT
 TTCTTTTGCCATCTGCTTTTTCATATTCCAAAACCTGGAGTTACAAAGATGATCAACAACGT
 ATAGAATGAGCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAAT
 GTTTTCAAATAATGTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTATTCTGATTTGAACCTCTGAACCCCTCAGCAAGTTTCAATTTT
 GTCATGACAAATGTGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAATAAAAA
 AA
 AAAG

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRKFTVPQINCVDKAGKIIDPEFIVKC
PAGCQDPKYHVYGTVDYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQ
RQDPGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHTNLKTHTNSTRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKFEISDSTDTRIGAVQYTYEQRLEFGFDKYSSKPDIL
LNAIKRVGYWGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

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FIGURE 114

CAGGATGAACTGGTTGCACTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTC
 TCCAGCCTTTTCCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCTTGAGGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGGTACCCA
 CTTCCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGCGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTCAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCCT
 AGACTCCTCATTAACCACTGGATAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

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FIGURE 115

MPFRLLIPIGLLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDVPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFQSL EAYWPGLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDP TLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNF IHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARP GT
LFSPENHDQARERKPAKQKVLLSCFSPFTSKLALLGQVFLDSS

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AAGTTACATTTTCTCTGGAACCTCCTTAGGCCACTCCCTGCTGATGCAAACTCTGGGTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGTCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTGTATGTGGAGCCAGTGATCGCGCCTGGAGA
 AACAGTGTACTATTCTGTCGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTT
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGCTGCATAGTGTGAAGGCCGACA
 CATTCCTGAAGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGTGGCAA
 GGAGAGGCCATTCCCTGGTATCTGGCCCTGTTTGCTTTGTTGGCTTCATGCTGATCCTGTG
 GGTCTGTGCCACTGTTCTGTCTGAAAAATGGGCCGGCTGTCTCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAAATAAACCAATTACCCAGAAAGTTAATCAGCTGCGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCTAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGCCCACTTTCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCCACTGAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATCGCAGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTCT
 TGTGGTAAAGTACAGAATTACGCAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

MQTFTMVLEEIWTSLMMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMMWSPVIAIGE
TVYYSVVEYQGEYESLYTSHIWIWSSWCSLTGEPCECDVTDIDITATVPYNLRVRATLGSQTSAW
SILKHFPFNRNSTILTRPGMEITKDGHFLVIELDLGPQFEFLVAYWRREPAAEEHVKMVRISG
GIPVHLETEMPGAAEYCKAQFTVKAIGRYSAFSQTECEVVEYGEAIPLVLALFAFVGMLRLV
VVPFLVWMKMRGLLOYCSKPPVVLPTDLKITNSPOKLSCREEVEDACATAVMSPEELLRAWIS

Signal peptide:

amino acids 1-29

amino acids 230-255

amino acids 40-43 and 134-137

amino acids 92-119

amino acids 232-262

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAAATGGTCTAGAGAAGAACTGGACAAGTCT
TTTTCATGTGGTTTTCTFACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACGAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACCTGATGCATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCGAGTTTGAGTTCCTTGTGGCCTATNGGAGAGGGGCAAGCCCTTGCGGCGCAAGGG
GTNNCGCAACCCCTGCGGCCGTGGGTATCTCTCGAAGAGGAGAGGCCCAATGATGCCAC
ATACTCAAATATGACGAANTGCTATGTGCACCTGTTTGAGTGGCGCTGGGTGTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGTGGCGGCGACGGTGGCAGCGCGGTG
GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGCGGG
TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCAGGCCTGCAGCAGCTGCAGCG
AGACCTGGGGCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAAGTTTGGCCAAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
TGGTAGGGGCTTGGGACCCAACTGTGTCACTGGAGGAGGTCAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATAACCACCGCGTCTCCTCCTCCACCA
CCTCATCCCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTCCTTTACTCTTATGCCATTGGTCCCATCATTCTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTTGGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATTATTTTCTTCAATTACAAAAGAAATGCAAGTTTCAATTGTAACAAATCCA
AACAATACCTCACGATATAAAATAAAAAATGAAAGTATCCTCCTCAAAAA

MVAATVAAAWLLWLAAACAQQEQDFDYDKAVNIRGKLVSLSEKRYGVSVLVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFPCNQFGQQEPDSNKEEESFARRTYSVSPFPMFSKIAVTGTG
AHPAFKYLAQTSKEPTWNFWKYLVPADGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GTCTGTCTACGTCGGGATGC
 TCGCCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTCTGGGGGCCCGGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAAGGTTGCCGCTTCCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCATCGGAGGCCCTCAGCTACGTTCAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCTTGGAGACCACAGCACAGAGGGTCCCAAGAACGAGAGGCC
 TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCGCGCCTCCTGAGCATTGGCCCTCTGCAAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGCTCTCAAGAAGTGGGTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAGAGCCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAAAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACCTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCCAACCCCTGTACCATGCGCTGGGTTCCGTGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCTCATCTGGCCCTCTCCATCTTCAATGGC
 AAGAAGGCAGTGGAGGCCATCAGCAGAGAGAGGGCACCTTCCTGTATGTTACCCCCAGAT
 GTTCGTGGACATTCTGAACAGCCAGCACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCGTGACATTGCGCACTT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCCTCACACGGAGG
 CCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAAGCTGAACAGCCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGCTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCCAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTCAGGTTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTGCATTCCGGCTGAAGGACGGGGAGGAGACCAGG
 TGAGGAGAGATAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAACAACTACCCCTCACCATTTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCGTGCTGGCCGGTTGGCTT
 GACTCTCTCCTGTCAAGATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCAGGTTT
 TGAGCCAGGCACATCAATGTGCAAGGAATTGACTGAACGAACTAAGAGCTCTGGATGGGTG
 CGGGAAGTCCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCCATTTCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

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FIGURE 122

MAVYVGMRLRLGRLCASSGVLGARAALSRWQEARLQGVRLSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPN SYAWVLMQLATAQAGIILVSVNPAQAMELEYVLKKGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPLDITTVISVDAPLPGTLLDEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGIAGSPAPPELIRAIINKINMKDLVVAAGTYTENSEPVTFAHFPEDTVEQKASV
RIMPHTEARIMNEAGTFLAKNLPGELCIRGYCVMLGGTVEPQKTEAEVADQKXYWTGDSV
MNEQGFCIKIVGRSKDMIIRGENNIYPAELEDFFHTHPKVQEVGVGVGKDDRMGEETACACIRL
KDGEETTVEIKFAFKCKGISHFKIPKYIVETVNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTCCTGGGTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

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FIGURE 124

GAGCAGGACGGAGGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGC GGGGTTGCGGTTCTGGGACTCCCCGGCAAGAATGACCGCGCCTGGATCTTACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCCGCGGTCTGTAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGTGTGTCCAGGATGAATCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCAACCCCTTGTCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCATGCCCAGCGCCAACCACTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACCTGGACTGGGCTGGCCAGCCCTGTTTTTCCACATTCCTCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCCGGTAC
 CCAATTCCGCCCTATAGTGAGTCGTA

MDPARKAGAQAAMIWTAGWLLLLLLRGGGAQALECYSCVQKADDDGCSPNKMKTVKCAPGVVDVCT
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQCCAQDRCAKNLNTSRAL
DPAGNESAYFPNGVECYSCVGLSREACQGTSPVVVSCYNASDHVYKGCDFGNVTLTAAANVTV
SLPVRGCVQDEFCTRDVGTGPGFTLSGSCCQSGSRCSNLDLRNKTYFSPRIPLVRLPFPPEPT
VASTSTVTTSAPVRPTSTTKMPAFTSQTQRGVGEHARSDEEPLRTGGAAGHQDRNSG
QPKAGGQPOPHNKGCVAPTAGLAALLLTVAAGVLL

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCTCTGACGCTGTCTGGCCCCATGGTCTTGCCAGTGCAGTGC**AAA**AG
GAGAAGGAAATGGACCTTTTCATTATGATTACCAGACCTGAGGATTGGGGACTGGTGTT
CGCTGTGGTCTCTTCTCGGTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGGCCCCAGAGATGAGGAAGCCCCAGGTGGAGAACCTCATCACCGCC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGGTGGAAGCCTCTGGAA
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCCCTTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCTCCCCACTGCAGCCTGCGGTCTT
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCCTTTGTGGTACTTGTTTGTGGATGGTATTGTGTTTGTGTAGTGAATGTGGACTGCTTT
CCCCAGGCGAGGGGTGAGCCATAGCCATAGCCATCTGCTCCCTGCCCGTGGCCCTTCATCAC
CTTGTCTGCTCTAGGAGGCTGCTTGTGCCCCGAGACAGCCCCCTCCCTGATTTAGGGATGC
GTAGGGTAAGAGACAGGCGCAGTGGTCTTCAGTCGTCTTGGGACCTGGGAAGGTTTGCAGCAC
TTTGTCAATCTTTCATGGACTCCTTTCACTCCTTTAAACAAAAACCTTGCTTCCTATCCC
ACCTGATCCCACTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTGAGGCAAGGCTATGCCCTTCCGTGGTTAATTTCTTCCAGGGGCTTCCAG
AGGAGTCCCCTCTGCCCCGCCCTTTCACAGAGCGCCGGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCTGGGGAATGTGTCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCTTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCGCTTGTCTTCTGCCTACG
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCCGTGGTCAGA
GCGGTGAGCGAGGTGGGTGGAGACTCAGCAGGCTCCGTGAGCCCTTGGGAACAGTGAAG
CTTGAAGGTACATAACGAGATGGGAATCAAGCCAGATCCCGCCCCCTGTCTCTGTGTGTT
CCCGCGTAACCAACCAAAACCTGTGCGCTGTGACCATTGCTGTCTCTGTATCGTGATCTAT
CCTCAACAACAACAGAAAAAGGAATAAAATATCCTTTGTTTCCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGLWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCATTTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAAGTCCAATAAAACATTTTCCATCCAAA

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FIGURE 129

MKIPVLPVVLSSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

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FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCTGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCACTATTAATTGTAACGATTAATAAAGAAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVLLQFVPTQETGPKAMGDLSCGFAGHS

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FIGURE 132

GGGGAATCTGCAGTAGGCTCTGCCGGCGG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG
 GCCATGGA AAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCAGAATACACCAAAAAC
 CAGGCCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTCTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAAATTAT
 TCCCAAAATGTTGAAAACGAACTA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTATTGCTGGAATTGTGAAATTAATCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCATGCGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCAATAAATCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWSMKDT
LGKPAAKDVHLVDHCKYKYLNFVRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKG YDQIIPKMLKTEL

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CACCCCTCCATTCTCGCCATGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
TCATCCTGGCCTTTGGCACCCGGAGTGAGATTCTGTCGCCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
GACTATGCTGAGCTCATGGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGCT
TTCCTCCTTACCCTCTACCTGGGCCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTTGTTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATCTGAGTTTCAGCCA
CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
CTGACCACCTCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCTTCTGCACCGT
GGCTTCCACTCCAAGAAGGTGGACAGGGCTGCAAGTCTCAACCGTCATAGCTGTCCCTCCA
GGCCCCAACCTTGCCCTACCACCTCCGGGCCCTAGACTTTCGACCTCCTTAGCGCTGCCCTCT
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCTGCTCTTAACTCGATGACTTGGGGTCT
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPILCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQODLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCTCGCTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGCTCTTTTTTCTGTTTTTCAGAGTAGTTACAAACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAAACAACAAAAAAGCTTAAGCTTTAATTTCTCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTCGCGTGTCTCTG
 AGCTGTGTGGATGCTCGCTCTCTGGACTGCTCTCCGAGTAGGATGTCACCTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACCGCTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTGTCTCATCAAATCCATTT
 CTGGTCACTTCTGGTGACCTCCCAACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGTT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC
 ATTCAGGTGGTAAGTGAAGTTTGGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATCTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTATCTCTAATTGATAATTATCTTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCTTTCAAGGTGTTCCCTCCATCTGCAGTGGGTGGGTTATATAA
 TGTCAGAGATTTGGTGCCCAAGGATCTATGAAATGATGGGTACAGTAAACCCATCAAGTTT
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAGAAGTGAACATTATATCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTATGCTAAGGAACACC
 ACATGCCATTATTAAGCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAATAATCATGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACGAACAAAATTTTACCTGTTTT
 TGGTCATTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATCTTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTGTGTAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAACTCGAAAA

MASALWTVLPSRMSLRSLKWSLLLLLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYIRQD
FHFTRLREHSNCSHQNPFVLIVLTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFFLLGQEA EK
EDKMLALSLEDEHLLYGDII RQDFLDTYNNLTLTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLNLNLNHSKFFFTGYPLIDNYSYRGFFYQKTHISYQEYFPKFVFPFYCSGLGYIMSRD
LVPRYIEMMGHVKPIKFEDVYGVICLNLLKVNIIHIPEDTNLFFLYRIHLDVQCRLRVIAAHG
FSSKKIITFVQVMLRNTCHY

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATCCATCTGGGATTATGGAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACAGCACCAGTGACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCCTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

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FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGKGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

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CAATTTCTGAAACTAAICGTGTGAGCAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
TTAACTTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGFGAAATATAAATAAGAGAAGAAAAA
GAATTAAGTAGATTGAGTCTCCAATTTTATGTAGCTTCAGAAGAACTGGTTTGTTTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCACCCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
TTGAATCCGGATGGAAGTCCAGCCCTTTCAACCTGGTGGATTTCCTCAGCTCCCAAGC
ATCATCACAAGAGAAGTAAAAGCTGAAGAGAAATACCAATCTCCATTAAGTGTGAAGCAG
TCAAAAAAGCAACCTGAGGATGAGACACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCAGC
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCGCCGAGTCACAGTGAAGCCCTCGAAGACATCATAATCAT
GGTTCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGTCTCTTT
GAGAGGTCCCATAAAGCAAGCACCATTGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGA

CTGACTTTCTCTCTCTTTGAGCTGCATCAGTTCTTGTTTTGCCTATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTTCTTGAAACCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAAGTGGAGCGTGAATTCGTAAAAATGTATCTTATTTT
ATACAGATAAAATGCAAGCACTGGTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
ACTTTCTTAACACTGGTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTCTAAAAA AAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRVKVALQEAQLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPI SINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSRRSRSRSRSHSESPPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKSRSRSQ
SKSRDHSDAAKKHRHERGHRDRRERSRSFERSHKSKHHGGSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTNTTATTGCTTACTGATTTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTCTTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGGATT
GAATCCGGATGGAAGTCCAGCCCTTTCAACCCCTGGGTGGATTTTCTCC

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FIGURE 143

GGCACGAGGCGCTCGTGCCAAAGCTTGGCACGAGGGTGCACCGCTTCTCGCACGCGCT**ATGGC**
 GGTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCTCGAGCTGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCGTGGCTGGC
 CCAGACCCACCGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTCACGGGAC
 TTCCTGCACAGCCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCTCTGCTGTGCTGGTGGTGTGCTGCTGCGCTGGCGGTGACCCGCCCCC
 ACCTGCAGGCTACCTGTGCTTGGCCAAAGGCCCGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCTGGT
 GAGCTTGCAGTACCTGACGCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCCCTTCTCTCCGTGGCGTCTGECCTACCTCATCTGGT
 GGACGGCTGCTGCCAGTGTCTCGCCAGCCTTTTCGGCTCTACTTCCACCAGCACTTGGCA
 GGCTC**CTAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCGCCCCGTGTCCTCCAGCTGCAAGGTGGGGCCGACTCCCC
 GCGGTTCCCTTACACACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

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MAVLGVQLVVTLLTATPLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCLPTTVDALVLRFFLEYQWVFDAFVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTIVRLYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTTPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFIWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSQYLTPILITLNCLLTLLTCTLGGSYWGSLGAPALLSPDPSSAAAPIGSGEDEVQQTAAIR
AGALGGLLTPLFLRGVLAYLWWTACOLLASLFGLYFHOHLAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

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GGTCTCTACATCCTCTCACTCTGAGAATCAGAGAGCATATCTCTTTCAGGGCCCGTGATTATTTAAAGCTGGCTT
AATCTCGAAGGTTCTCAGTCACTTAATCTTTGTGATCTCTACTGATTTCTGGGGCATCGCAAGGTTCTGTAAAGAGCG
TTGGCTGGTTTGGGCGCTTTGAGTCTGACAGAGGTGGCCAGGGAGAATCAGCACACTCTCGGAGATCAAGAGC
CGCTTCTGTGTTGGTCTTGCTTGTGGCTCAGTCTCTGTAACATCTGACATCTGGGCACTCTCACTCTCTG
TATCTCAAGACTCTTAAGAGTGCTTCCCATCGGGCTGACCAAGATAGGAAGGGCGCTCACAAAGTGGCTG
TCGACAGCGGCTGTGCGAGCTCACAGCCAGGCTCTCCCTCCGACAGGTTCTGTCAGCTCTGCCACATCTCTTA
TCAGACAGGAGCTGCGCTAGACACCTGCTACTGTTCTCTCGGAGAGGACGGGACGCCAGCACTAAGCGC
GTGGACTCTGGCCGGAGCACCGAATAGGGCAGCGGCTTTGAGAGATCCATATAGGAAGCAGATCACTTAA
AAAAATTAATCAGAGCTTTGAGTTGTTCTTCAAGGAACAGAGCGGGAGTCAGTTTGCACACCTCCCGACAGG
CTAGGAGAAATTTCTGAAACACCACTCGCCCTGAAGTCTTTCCCAAGTGTTCACCCCTGTTCAGATGTGTAA
GTCACCAATCAAGATCAATCGAGTAGTACCGAGTGAAGCGCTCTATTAGCTGTGGGAGGTAGCGAAAC
CCCACTGTGTCATATCATTTATCCACACATTTATCTGATGGGTGATCGCAGAGAGCGGCCGCTCTGCGAC
GAGACATCATCTAAAGGTCAAGCGGATGGACATCGAATCTCCCTCAACATACGCTGTGTGCTCTCTCTCGGG
CAGCCCTCGCAGGTGCTGTGGTGACTGTGATGGTGAACAGAAAGTCCCGCAGGAAACATGGACAGGCCCC
GGATGCTTACAGACCCCGAGTACAGCTTTCTATGTTTCTCAACAAAGTAGCCCCGAGGAGCGCTTGA
TAAACTGTGTCGCAAGGTGGATAGCTCGTGGGTTTTCATCTCAATGTGCTGATGGCGGTGTGGCATATCGA
CATGTTGACGTTGAGGAATGACGCTGTGTAGCCATCAATGAACATGATCTTCGATATGGCAGCCGAAG
CGGCTGCTATCTGATTCAGGCCATGGAAGACGTTTCACTCTCTGTTCTGCTCCCGACAGTCTCGGCAGGGCC
CTGACATCTTTCAGGAAGCCGCGTGAACACGAATGCGAGTGTGCTCCGAGGCGAGGGAGAGGACACACT
CCCAAGCCCCCTCATCTCAATACTTCTTCTGATGGAAGAGTGGTAAATATCCAAAGATCCCCGGTGAATCT
CGCGATGACCGTTCGAGGGGGAGCATCATAGAGATGGGATGGCTCATATGTGCTACAGTGTGTTAGCCGC
GAGGATCTCATAGCAGAGATGGAGAAATAAAAACAGTACATTTTGTGAATGGATGGGTGCGAATGACA
GAGGTGACGCCGAGTAGGCGCATGTGCATTTATGAAAGAGCATCATCTCGCTAGTAGTCAAAAGCTTTGGAAGT
CAAGAGTAGTAGGCCAGGAGGAGTCTGAGCGACCGCCAGCGCCCTGGACTCAACACACAACTAGGCCCCACCA
GTAGCTGTGCCCATCTGTGGTCTGCTGGTGAATTTACCGGTGCTGTGATTAAGTATTAAGAAATTTGATTA
CGAGAAAGACAGCTGAAGTGTGGGTTCTGCAATGTAGGAGTTATGAAGATACAAATGAAACAAACCTTT
TTTCACTCAAACTCATTTGTTGAAGGAACACAGCATACATGATGAAGATAGATGTGGTGTATTTCTTTCT
CTGTCATGTGTAAGATACATCAGGAATACATACATGCTGCTTGCAGCAAGTCTCGTGAAGAGTCTTAAAGGA
ATTACTCTAACTATGTTCTTGCCCTGGCACTTTTTTATAGAACTAATGATGGTTCAGAGGAAACAGAAAA
TCACAATAGAGCTAGAGATGAACACATATATTTATCTGCAAGTTTTATTTAAAGAAAGAAATACATGTT
TAAATCTCGAGAAAGTAGTATCATCTAAATGAAGCGAGTACACTCAGAAAAATATGTTTCAAAAAAATTA
AAACTCATGTTTGTCTTCAGTGTGGAGGATTTCTCATATCTCTCAACATCTGTTATATTTTCTTCAAT
AABAAGCCCTAAAAACCAATAATGATGTTTGTATACCCCATGAATCAAGCTGATTTAAATTTTAAATTT
GGTATATGCTGAAGTCTGCCAAGGCTACATATGGCCATTTTAAATTCAGACTAAATATTTTAAATGCA
TTGCTGAGAAAGCTTGCTTTCTCAACCAAGATAAATTTTTCAGAACTTAA

FIGURE 147

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MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHD LRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRTAGSLGFCIV
GGYEEYNGNKFFFIKSIVEGTPAYNDGRI RCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCTCTCCCAGGCAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATTTCTTTCCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAAATATAAATGCTGTATTATA

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FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAGTCTGAGGTTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTCCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCCAGCCACCACGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAGCAGCAGCCATG**TAGA**ATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA
GTTTCATGCAAAATGAGTGTGTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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GGTCTCTTA**AATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCC GGCGTGGGCGAGCCGACCCTCACTCTCTTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTACACCTGTCACTCCCTGGGGAAGAAA
CTAAATGTACAAACGGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTTCAGT
TTCGATGGGCACTCTTCTCTCTTTGACTCAGAGAAGAAATGGGACAACGGTTTCATCC
TGGAGCCACAAGATGAAAGAAAAGTGGGAGAAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTCTTTGATGGGCATGGACAGCACC
CTGGAGCCAAAGTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGACCCAATAGCTCATTCAGTGCTTGATTCCCT
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACCTAAAGTTCCTGGCTGACTAAACAAGATATATCATTTTCTTCTCT
TCTTTTGTGTTGGAAAATCAAGTACTCTTTTGAATGTGATCTCTTTCTGCAAAATGATT
GATCAATAAAATAATCAGTTAGACTTAGACTTCAGACCTCTGGGATCTTTCCGTGCTCTGAAAGAG
AATTGTTTAAATATTATTAATAAGAAAAAATATTATTAATGATTGTTTCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCTCCAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRGPRWCAVQGQVDEKFTL
HYDCGNKTVTPVSPLGKKLNVTAWKAQNVLREVVLDLTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQSFDFDQIFLLFDSEKRMWTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

GGGAAAGCCATTTCGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGGA**ATG**GAG
TTGATCCCAACCATAACATCGTGAGGGTTTTAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTTCTTTGAGAGGATTCCACCTTCAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCCTCCCATAAACAGGACAGATTATTCAAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTTGGGAGGCCAAC
CCACAGAACAGCATTCTGGGCCAGGCTG**TAA**TCAGAATTGTGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACCTCTCCCTTTACCTTT
CCTCTCTCATTACGATTCACCAAGTATATTTTCAATGAATTAACCTCTGCCAAGGGACC
TTAGATAGGCTTATCTGACTGTATGCTTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTTTCAATTTTGAIAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

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FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACCTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTGGTCTTA
 CCTACCGGCCCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGGCCCC
 AGAAGTGGCCCTCCGTTTGTCTCGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCGCCACCTCCACCACCTGGAGGTCCTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTCAACCGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTG
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTCCATGGCCTGAGCTCCCTCAAGAAGCTTGGGTCTATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTACGGGCTGGCTTCACTTGTGGAAC
 CAACCTTGGCCCAATAACCTCTCTTCTTGGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTCTGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCTCT
 TCATCATGGAGCGCACCTCGAGACCTCAACATTTCTGAGGGTCCGATGGCAGAAGCTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTGTCGCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACAGTGTCTGC
 TTTGAGACACTGGGGGTACACATGCATGGTGACCAATGTTGACGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCTTA
 CCACGTCCACTGGTTACGAGCCGGCATATACCACCTCTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACCTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACACGAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATT
 ATGACCATATTAACTACAACACCTACAACACAGCACATGGGGCCCACTGGACAGAAAAACAGC
 CTGGGGAAGCTCTCTGACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGCCCA
 TACCAAGGCAAGGTACAGGAACTCAAAT**TGACT**CCCCCTCCCCAAAAAACTTATAAAAT
 GCAATAGAATGCACACAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTGA
 TATGCTTATATATTAAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTTAAATTTAAAGA
 CAAAAGTCAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLEFNLYNLGMCNIKDMPNLTPLVGLEELEMSEGNHFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHNPWNCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRLVEVDQASQCSPAFFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVTMVTNVAGNSN
ASAYLNVSTAEINTSNYSFFTFTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAATAAPSGVSGEGAVVLPITIDHINYNTYKPAHGAHWTE
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

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[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAERNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
QLYSAAFSKQKLQSAPTKKPALPFGDLPBGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAIIYRRTSKVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSFQESHITVAGWNVLADVRS PGFKNDTLRSG
VVSVDVSLLEEQHEDHGI PVSVDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLVSWSYDKTCSHRLSTAFTKVL PFKDWIERNMK

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FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCACTCAAGTTCGCAATCAGATTGGAAGCTCAACTTGA
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATATTACAGTAATAAAAAAC**ATG**GGC
 TTCAACCTGACTTTCCACCTTTCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTCTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAACCTGTCTTCTGTGTCTCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAAATGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCCAGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTTCTGGTTGGTGCA**TGA**CCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGCTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTATTTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTCAGGTGAGAAGCGCTCCACAAAAGAGGGGAGAAAAGGCAGCAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA
 TGCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLI FKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNRREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTA LSREQFFKVNG
FSNNYWG WGGEDDDLRRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVEHNPLYINITVD FWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

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FIGURE 162

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCGAGGAGCGACCGCGCAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGCCCCGCA**AATG**
 GCCCAGGCAAGTGTGGTCGCGCCTCGGCGGCATCCTCTGGCTTGCTGCTCCTGCCCTGGGCG
 CCGGGCAGGGGTGGCCGCGAGGCTGTATGAACCTCAATCTCACACCCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCTGTGGCCAAAGGACAACGGCAGCTGGCCCTG
 CCCGTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCCGGGGAATCCCCGG
 TCTCTGTCTGGGTCACTGCCGTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCTCCCCATCACAGAGTTCTCGTGGGGACCTTGTGTGCCACCAAGAACTTCCCTACC
 CTGGCCCAAGTCTCTATCTCACTAAGACCGTCTCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCAACCGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGTGAAGCTCGAGGAAACCTTCGAGGCATCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAAGTTCCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCCTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGACTAC
 TGCTTCAGCATCCGGGCGAGAATATCATCAGCAAGACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTGTCTTCCATGTGTACACTTATCACTGTGA
 TGTGTGGCCTTCATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAAGTGCTGTGCCAGATGTGTGTGGGCCCTTCTGTGT
 GGAGACTCCATCTGAGTACCTGGAATTTCTGTGAGAACCACGGGCTGTCTCCGCCCTCT
 ATAAGTCTGTCAAACTTACACCGT**GTCA**GCATCCCCCTCCCCACCCCATCTCAGTGTTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTTATT
 TGCGTGGGGCTGTGGCCTGGATCATCCATCCATCTGTACAGTTACGCCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTATACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTCCGTGTGACTCCTAGGTGGGCTGGCTGCCACTGCCCATTCCT
 CTCATATTGGCACAATCTGCTGTCCATTGGGGGTCTCAGTTTCTCCCCAGACGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAAGGTCTATAAAGGGTTAAAAATCCATACTAAAGGTTGTAC
 ACATAGTGGGCACACTCACAGAGAGAAGTGTGCATGTACACACCCACACACACACACA
 CACACACACAGAAATATAACACATGCGTACATGGGCATTTAGATGATCAGCTCTGTA
 TCTGGTTAAGTTCGGTTGCTGGGATGCACCTGCCTGACCTAGAGCTGAAGGAAATTTGACCTCA
 AGCAGCCCTGACAGGTTCTGGGCGCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTGAGTGATTCGACAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG
 AAATTTTCACTGAGGAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGGG
 TGGCTCACGCCCTGTAATCCACCACTTTGGGAGGCCGAGGCGGGTGGATCAGAGATCAGGA
 GATCGAGACCCTGGCTAACACCGGTGAACCCCTCTCTACTAAAAAATACAAAAGTT
 AGCCGGGCGTGGTGTGGGTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCCAACCCGGGAGGCGGAGCTTGAGTGAGCCAGATGGCGCCACTGCACTCCAGCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

MAQAVWSRLGRILWLACLLPWPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPEGEFPVSVMWTAADCWMCQPVARGF
VVLPITEFLVGLDVVTTQNTSLPWPSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYNYNSIIGTFTVVKLVVAEWEVEEPDTRAVKQKTGDFSASLKLQETLRGIQVL
GPTCLITQFQKMTVTNLFLGSPPLTVCWRLKPECLPEEGECHPVSVASTAYNLTHTFRDPGD
YCFISIRAENISKTHQYKQWPSRIQPAVFAPCATLITVMLAFIMYTNLRNATQQKDMV
ENPEEPSGVRCCOMCCGPKLLETPESEYILVRENHGLLPPLYKSVKTYTV

Signal peptide:

amino acids 1-24

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
GGGCCGCTTGCCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
CAACAGACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAGA**ACCTACCTGCCCTG
CCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCTTTTGTTCACAAA
AAA

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FIGURE 165

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCCHRSKCGMCCKT

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FIGURE 166

CTGT CAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCTCTTACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGGCTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCCAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGTTAGGAGTCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTCGGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTACAGAGAGCCATGGGTGAAGGCCCTG
 CCCACACGTCTGGTTTGAAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGACGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTCG
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACCAC
 AAGGACAGGAGCCGCTCCT**TGA**CGCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTGTGCTAGAGAT
 GGGGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCG
 CTCTCAGGAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCGACATGATAGGAAGGAACTGTCTGTCGAGGGGCTTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAAGCTGTGTTTCGTACTCCAGGCTAACCTGAACCTCCCC
 ATGTGATGCGCGCTTGTGTTGATGTGTGCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTGATTCCTACCTCACAGGCGTGTGTGGGGAATAAAGTGTCTGCGGGTGAGTGA
 AGGACACATCACGTTTCAGTGTTCAGTACAGGCCCAAAAACGGGGCAGGCGAGGCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

MFLLLPFDLSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLLEEIKEIRRGSSKALDNTPEFELSDIFYFCRKQME
TIMDEVTKRFSAEELSWNLLSRTYNFQYISRLTVLWGLGVLI RYCFLLPLRIALAF TG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRLTAIITYHDRENRPNGGICVANH
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLEHVQ
DKSKLPILIFPECTCINNTSVMMEFFKGSFEIGATVYPVAIKYDPQGFDAFWNSSKYGMVTYL
LRMMTSWAIVCSWYVLPMTTMADEDAVQFANRVKSATARQGGLVDLLWDGGLKREKVKDTF
KEEOOLYKSMIVGNHMKDRSR

FIGURE 168

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLILLAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCTCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTCTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCTCATGGTCCCTGTGTCTCCTGTTGGTGCCCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

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FIGURE 171

MAGSPTCLTLIYILWQLTGAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVITMGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCT
GTGTCTCCTGTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA
AGATGGAATAATCCCCACTCACTGCTCAGGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCTTATCCATACAGCATCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCTTGACAAT
TTTTCATGAATATTCTCTTCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTATAGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

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FIGURE 176

MTCCEGWTSNCGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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FIGURE 177

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAATTAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCTC
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACATGCCGCCGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAACGTGGTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCTCGGATGCTGAC
 GCGCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGAGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGGCGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTACAGACGCTGTTCATCCGGGAGCGCGCTCG
 CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTCAATTGATGTGCTTCGTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 TGGGTCTGTACAACCTTGCAGGCCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
 TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC
 CGCAGGGGCCAGGAAGTGCATCGGGCAGGCGTTCCGCATGGCGGAGATGAAAGTGGTCTCG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGCTTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA
GTGACTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTCTCAAA

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FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRQLQCFPPKRNFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDITRSITNASAAIAPKDNLF
IRFLKPWLGEIGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
SRLDMPFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGAAAAATAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDSDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGTTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAACGACAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAAC TGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTT CAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG TGATCGCCCAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGCGAATAAATGTTCAAAC TGTA

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FIGURE 186

MPSPGTVCLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTGTGTATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAAGGTGAGCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCAGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTACA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTTCAACAATGAAATATATTACAGGCAGGTACCCACTAACCA
 AACAACCTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTGGAAGT
 AACAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACAAGA
 GCCTCCTTGTTTACATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIGMLVLLLDLGLVHLGQLLIFHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCTTCTCTGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCTGTGCCAGAAAGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGTTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTATCAGCTTCTCCTGTCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
 GGCTTCTACATGGCCTGGCTCTCCTTCACTGCTGCATGGCGTGGCTGTCAACCACCTTCA
 ACAGCTACACCAGGATGGTGTGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTCCTCGGGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACAGTATCATAATCAGCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCACTCTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGATTCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCACTTGTGTTTACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWVFVGTQVKVPKPLECKGLAAKCFDMP
VSLDGDNTSTQBEVVQYNWETGDDRFSRFSRSGMWLSCETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPFPLGLCGKNPMVIPGNADHLHRTSIHQ
LPATNRLATHWEPQLAQTERLCCFLCPVRSPGDGGPHDVTSLSPSDCLGSRRLTETCLE
LWLGLHLGLALLHLHGVGCHHLQHVVHQDAGAGVQQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTCTATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCCTATTCTCTCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCCTCCCCCTGCCCGCGTAGATTTCAG
GACATTGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAAA
GGGAAGCAACAGGAACTTCTGCAACTGGTTTTATCGGAAAGATCATCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGTCTCCGGCTGCGCGTGTGCGCGCGCGCTCGGGTCTGGAGCGCAGGAGCGACGTCA
 CCGCCATGGG CAGGCATCAAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTT
 GGATGTGCCCTTCCAAATATACAACAACTACTGGCCCTCTTTGTCTATTTTACATCCTTTACACTATCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGAAGGAAGTGGCAATCTTTC
 TTACAACGGGCACTTCTCTGTGAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCAATCTGATTGAGTGGGA
 GCTTTGTGCACTTGTCTCTCAGAGAAACAGACTCATCTTGAACATATACAGGCTCTTTCTGGCTTTGGGAAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGA¹AAAGAAATTACTGAACATTTCTCAATGGACTTCTGTGCTATT
 GTTGGCCATTCACGCACACAGGAGATGGGCGATTAAATGCTGAATGTTATAGCAGGCTCTTGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGTCTGAAGGATTAAGGATTTTCT
 CTTTTGGAAAAGCTTGACTGATTTACACATTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTAGTTGATTTTGTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGT TAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATATT
 TAGCCTCCATTATTAACAAAAATTAATAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTAAATGCCCATGCCCTCCGTAAAGGTTGTGGTTTTACTGGTAGACAGATGTTTGTGGATTG
 AAAATTTATTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTTGTAGAAGAATTTATGTTAACTTTA
 AGGTAAGGTTGTAACAAACATTTTGAAGATAAGGTTTTTATTATGTTTATTATTTGTAGAGTGAGTGCATGT
 GGGAGAAGATGACATTGAATTCAGTTTGAATCCTGTTCTATTATTAAGTGAATTTGTGATCTCCTATC
 AACCTTTTCATGTTTTACCTGTGTTAAATGGACATACATGGAACCACTACTGATGAGGACAGTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTAAATACACTAGAAGTGTTTACTTACCTGGAAAAATTTGCTATGCCGTACATT
 CAGAGTGCCCCCTCCCCTGCAAGGCTTGCCATGATTAACAAGTAACTTGTAGTCTTACAGATAATTTCATGCA
 TTAACAGTTTAAAGATTAGACCATGGTAATAGTAGTTCTTATCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTAAAGCAAGTTTCTCTGTATACCTCTGAAGTGTGTTGATTGAGTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCATTTGTTGTGAGTTAATGCAAAGTAGCCAACTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATCCAGTAGCCAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTTACAGGA
 CTTTTCAGAGTGGGTTATAAACAATTCAGTTGGTCTGACAGTATTTGTTAAGGATATTTGTTGTATG
 TTTATTCAGTATACTACATAAAAAATTTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGCTGTGTT
 TTTATGAAGTTTATTTCTCAGAAAAATGGGAATAAATTTGGGATTTGTTGAGCTTTTACTAAGATGCCTAA
 AGCCACAGGTTTATTGGCTTAACCTTAAGCCATGACTTTTATAGATATGAGATGACGGGAAGCAGGACGAATATCG
 CGCTGTGCTGGAGCTTCCCACTGGAGGCTGAAGTGGCTTGTGGTATTATAATGTTGAGTTTCAAGAGGA
 GGTG CAGGTACACATGCAATTAGAGAGCTGGTGACAGTGGGAACCTTTGTGCTGTGATCTACTGGACTTT
 TTTTTG CAGGAAGTCTCTGCTCTCCCTATTTTCTGTTCTGGATGTCAGTGCAGTGCATCTGCACTG
 TTTTATCCACTTGGGCCACAGACTTTTCTAACAGCTGCGTATTTCTATATCAATTAATTCATTCGACAGATT
 GTGCTTTGACCTTGATCTAGCTTTGACATAGTGTCTGCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGATATGCACTGATACACATTACCATTCTTCTATGGAAGAAAACTTTTGTGATGAACATAA
 AGATTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQQTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRLLSLHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRITYIEPRILNSWKSITSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEYYVDYKPNH
IEGALVIINEYGSCATCHQQPARECEV

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPDGLV LASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACCTATCTTCTGCATTTTGCACTCTTTGGCA
TTGACGTGGTACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGC
CGTGTGCTTTGCATTAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACATGGACAGAAG
CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTCTGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT
TCTCGAACCTGAATGTCTAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
CTATTACGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCTCCAGTCAACCCTCCGCGCGTTACCCGCGGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCTCCCTCCCGTTGCTCCAACTAATACGCACTGAACGGGATCGCTGCGAGGGT
 GGGAGAGAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG
 ARCTGATCAAGTACTTTGAAATGAGCTTCGAAATTTATCTTGGTGCCTTCATACCTTGCCTGCACTGGATCTTTC
 AACCACTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGTATGGATTCCGTTGCGGATTA
 TATATAAAGTTTCAACGCGCCCATTTTTCATTATATTATGAAATATGGTGTTACCGTGAAGCAAGTTTACTAATGTT
 TTTATTACAAAAACCTACCTTAACCATTATACTTTGGTAACCTGGCGCTCTTTGACAGAGAATCATGGGATTGTTGC
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTT
 GGGAGAGAGCGACCAATATGGATCACAAACCAGAGGGCAGGCATACATAGTGGTCAGGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTCTACTCATTACATGCCTTACAAATGAGTCAGTTTCAITTTGAAGATAG
 AGTTGCCAAAATTTGTTGAATGGTTACGTCAAAGAGGCCATAAATCTTGGTCTTCTATTTGGGAAGACCCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCTTTTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAAAGTGATCATGG
 AATGACGCACTGCTCTGAGGAAAGGTTAATAGAACTTGACCACTACCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAATCAACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTTACAGAAATAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTGTAGCCCATGGTCTGCTTCAGAAAGAAATTT
 TCAAAGAAAGCCATGAATCCACAGATTTGTACCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATACTCCTCCTGGTGTGTTAAACAGCAGAAATATGACCAAGAGGGGTCAATACCTTATTTATAGGGGCTC
 TCTCTTGGGACATTATAGTGATTGATTTTGTATTTTCAATTAAGCATTAAATTCAGAGTCAAAATACCTGTC
 CTTACAAGATATGCATGCTGAATAGTCTCAACCATTTATACAAGCCTAATGTTACTTTGAAGTGGATTGCTATA
 TTGAAGTGGGATTTCCATAATTTATGTCAGTGTTAAGGTTTCAAAATCTGGGAAACCAGTTCCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACACACACACACACACAGGACCAAA
 ATACTTACACCTGCAAGGAATAAAGATGTGAGAGTATGCTCCATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTATTTGGAGCTTGGCCGAGATATGTATATTTAGCAACTTTGCATATGTAAGTACCTTTATAT
 ATTGCACTTTAAATTTCTCTCCTGTATGGGTACTTTAATTTGAAATGCATTTATGGACAGTTATGTCTTTATAAC
 TTGATTGAAATGACAACTTTTTCACCCATGTACAGAAATACITGTTACGCATTGTTCAAATGAAGGAAAT
 TCTAATAATCCGAAATATGAACATAGAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTGA
 AAATTAATATGATAACCTTTGAACCTTGAATTTGGAGATGATTTCCCAACAGCAGAATGCAACTGTGGGCAT
 TTCTTGCTTATTTCTTTCAGAGAAGCTGGTTTTCAATTTATTTTCCCTCAAAGAGAGTCAAATACTGCAG
 ATTCTGCTAAATATATGTTTCTGTCAATAAATATTTGTGATTTCCCTGATGAGTCATATAGTGTGATTTTCA
 TAATAATGAAGACACCATGATATCTTTCTCTATATAGTTCAGCAATGGCCTGAATAGAGCAACCAAGCA
 CATCTCAGCAATGTTTTCTCTGTTTGTAAATTTTGTCTCCTTTGAAATTAATCACTATTAAATACATTAA
 AATCAAAATTTGGATAAAAAAAAAAAAAAAAAA

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FIGURE 202

MTSKFILVSFILAALSLSLSTTFSLQLDQQKVLVSVFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW
 ITNQRAHTSGAAMWPGTDVKIHKRFPHTYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTNLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

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FIGURE 203

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAC TGCGGGAGGCCAG
 GACAGGCCACCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTTGCCCTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCAACCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCTTGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCACACACAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCCTGCCCCGACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTC TGATGCCCTCCTGGTG
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCTCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCTCTGTTCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTT CAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACTTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCCTGAAAGTCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDDYHAWNINYYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGLRLKLFSSHRFQVIIICLVVLDALLVLAEILDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCAGCAGGCCGCCAACAT
 GCTCTGTCTGTGGCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTTG
 AGTCCGAAGGGGCTCCCTGGCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCACTCCCTCC
 CAGGAATTTCTCACCTACCAGGCGAGTGGAAAGCAGAAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCGAGCTAGACTTTGAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAGCTGA
 GGCTGGTGTTTAAGATTTTGGACAAAAAGAAATGATGGACGCTATTGACGGCGAGGAGATCATG
 CAGTCCCTGCGGGGACTTGGGAGTCAAGATATCTGAACAGCGAGGCAAAAAAATTCTCAAGAG
 CATGGATAAAAAACGGCAGGATGACCATCGACTGGAACAGTGGAGAGACTACCACCTCCCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCTCTAAGGAGCATTCCACGATCTTTGATGTG
 GGTGAGAACTTAACGGTCCCAGATGAGTTTCAAGTGGAGGAGAGGCGACACGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACTGCACGGGCCCCCTGG
 ACAGGCTCAAGGTCTCATGACGGTTCATGGCTTCCCGCAGCAACAACTGGGGCATCGTTGGT
 GGCTTCACATCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA
 CGTCTCAAAATTTGCCCCCGAATCAGCTCAAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACACGAGGACTCTGAGGATTCAGAGAGGCTTGTGGCAGGGTCTTGGCA
 GGGGCACTGGCCGAGCAGCATCTACCAATGGAGTCTTGAAGAACCCGGATGGCGCTGCG
 GAAGCAGGCGCAGTACTCAGGAATGCTGGACTGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGCCTTCTACAAGGCTATGTCCCCAACATGCTGGGCATCATCCCTATCGCCGGCATC
 GACCTTGCAGCTTACAGAGAGCTCAAGAATGCCTGGCTGCAGCATATCAGTGAACAGCGC
 GGACCCCGCGGTGTTTGTCTCTGGCTGTGGCACCATGTCCAGTACCTGTGGCCAGTGG
 CCAGTATACCCCTTGGCCCTAGTCAGAGCCGGATCAGGGCGCAAGCCTTATTTAGGGCGGT
 CCGAGGTGACCTTGTAGCAGGCTCTTCAAAACATATCTTGGCGACGAGGGGGGCTCTGGGCT
 GTACAGGGGGCTGGCCGCCAACTTCATGAAGGTCATCCAGCTGTGAGCATCAGCTACGTGG
 TCTACGAGAACCTGAAGATCACCTGGCGCTGCAGTCGCGGTGACGGGGGAGGGGCGCCCG
 GCAGTGGACTCGCTGATCTCTGGGCGCAGGCTGGGGTGTGCAGCCATCTCATCTGTGAATG
 TGCCAACTCAAGCTGTCTGAGCCAAAGCTGTGAAAACCTTAGACGACCCCGAGGAGGGT
 GGGGAGAGCTGGCAGGCGCTCAGGCTTGTCTGTGCTGACCCAGCAGCCCTCCTGTGGTTCC
 AGCGAAGACCAAGGATTTCTTAGGCTCCAGGCTCAGCAGGCTCCGGGCTCATGTGTAA
 GGACAGGACATTTTCTGCAATGCCCTGCCAATAGTGAGCTTGGAGCTTGGAGCCGGTTAGT
 TCTTCCATTTCACTTTCGAGCCAGCTGTTGGGCCAGGCCCTGCCTCTGGTCTGCGCTGC
 ATCTCCCTGTGCCCTCTTGTCTGCTGCTGTGCTGAGGTAAGGTGGGAGGAGGGCTACAG
 CCCACATCCCAAGCCCTCTGCTCAATCCCAATATCCATGATGAAGGTGAGGTACAGTGGGCT
 CCCAGGCTGACTTCCCAACTACAGCATTCAGCCCACTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGAGTCCAGGGGCTCGGGCTGCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCA
 TGGTGTCTGTAGCTGGCTTGGACCTGTCAAGATGGGCCCCACCTCAGAACCAAACTCACTG
 TCTCCACTGTGGCATGAGGGCAGTGGAGCACCATTGTGGGGCGAAGGGCAGAGCTTTGT
 TGTGTTCTGGGAGGGAAGGAAAGGTGTGGAGGCTTAATTTATGACTGTGGGAAAAGGG
 TTTTGTTCGAGAGACAGACCGGCACAAATGAGCACTTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTGTCTCAGAGTGTGTTCTGAGCGCTGGGGTTCTCTGTCCAACC
 CCAGCAGGGGCGCAGCGGAGCAGCCACATCCACTTGTCTCAGTGTCTGCGTCCGACTATTT
 ATTTTGTATTTTATTTGAACAGAGTTATGTCTTAATTTTATAGATTTGTTTAAATTAAT
 CCTTGTGATTTTCAAGTTTCACTTTTATTCATATTTATGTTTATGTTGATTTGACTTCC
 AAGCGCCCGCAGTGGGATGGGAGGAGGAGGAGGAGGAGGGGGGCTTGGGCGCTGCAGTCACT
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAGGCGACGACCCGTG
 GCTTCTTCTTCTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCTTAGGATTTACGGGTTTGA
 CTGGGGGCTGGAGAGAGGAGGAGAACCTCAATAACCTGAAGGTGGAATCCAGTGTATTTG
 CTGCGCTGCGAGGTTTCTTTATTTCACTTTTTCTGAATGTCAAGGCAGTGAAGTGCCCTCT
 CACTGTGAATTTGTGGTGGGGGGGGCTGGAGGAGAGGTTGGGGGCTGCTCGCTCCCTCC
 CAGCCTTCTGTGCTGCTTGTCTTAACAAATCCCGGCCAACTGGCGACTCAGGCTTGCACCTCC
 ATTCACCAAGGATACCTGATGAGGAATCTCAATAGGATGCAAAAGATCAATGCAAAAAAT
 GTTATATATGAACATATACCTGGAGTCGTCAAAAGCAAAATTAAGAAAGAAATGGACGTAG
 AAGTTGTCAATTTAAAGCAAGCTTCTAATAAAGTTGTTTCAAGCTGAAAAAATAAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEATFEQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLQMVASRSNNMGIVGGFTQMIREGGARSLWRNGI
NVLKIAPESAIKFMAYEQIKRLVGSQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAAFYKGYVPNMLGIIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCGCTGGGAACCTTCCCCAGCCAT
GGCTTCCCTGGGGCAGATCCTCTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTTCAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCGATGGTTCCTCCCGAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAATGTGACCA
 TGAAGGTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGCGCGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAAG
 CATGCAAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCAATGTGAACTAGACAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

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 10611126660

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIIITSKGKGANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESIARR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

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FIGURE 209

GAATTTGTAGAAGACAGCGCGTTGCC**ATG**GCGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGTGGCAGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC
 AGCGGTTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCTCTTCTTG
 AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCTGGCTGTGCCATCTGTAACCTCTCTGGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTAGTTCCCTCCCAGAACCCAT
 CTCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTCCCTCTGCAGCTGTTTT
 GCTTCCCTGTGGCCATCAGAGTTCCTTCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG
 GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCCCTCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCCTCTGATTCTTGCTATTATCCCAGGAGCAGTTGCTGGCAT
 GGTGCTACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC
 AACAGTCTACCCCTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCCCT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAAACAGAGTGAAAG
 AGTTTGTAAACCTTCAAGTGCTGTTCAGCTGCGGGGATTAGCACAGGAGACTCTACGCTCA
 CCCTCAGAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
 CCAGCTGCATGGAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGAAGAAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAACAGACAAAAAAAAAAAAA
 AA

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPF
LNQCGSLLYLTLASTDLTAVPICNSLAIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPIPLFFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 211

CTTCTGTAGGACAGTCCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCA**ATGA**AGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAATTCCTGTGCTGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGTGAAAGGCTGTTT
 CAACGTGAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAAACAAGACTCTTGAGGAGTCA
 TCTTTGAAAGTTTGTAGTGTGAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCC**TGA**AGGTCTGGGGCTGCACCTTGCCAGCACCCATTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSLET PVR
LYQNMFCSAENCSEETHITAFTVHVSAAEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKFPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

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FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCTCTACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCTCCGCGCCG
 GCGCGCTGCTGTGGTCCCTGCTGCTGAATCTGGGTCCCGGGCGGGGGGCCCAAGGCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCTGGCAGTCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCT
 TCAGATTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

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FIGURE 214

MVPAAGALLWVLLLNLPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINEEDEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQPCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNLSVVFTEMQPIDRNQR

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FIGURE 215

CCCGGGTCGACCCACGCTCCGGGGAGAAAAGGATGGCCGGCTGGCGGCGGGTTGGTCCTGCTAGCTGGGGCA
 GGGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAGCCGGTACCGCGACTCGGTACTGCGAGTGGGAAGAGCA
 GAACTGCTTCTGGGGCGCTCTGAATCACTTCCGCTCCCGCGACCAATCTACATGAGTCTAGACGCTGGACCT
 GTCCGGAGCACTTAAGTATGAGTGATATGGGGTCAACGTTGGGCTCTACCTCCAGAAAGGTACAAAAGTGCCCT
 CAGTTCCTATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCTGTTCT
 CAATGGCTGGCCAGCTGGTGATGCTCTGCGCGTACCGACACTTCGTGGCAGCCCTCTCCGCCCATGTACACCA
 CTGTGTGGCTTCGCGCTGGGTGTCCTCAATGCATGGTTCTGGTCCACAGTCTCCACACCCAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCGCTCCACTGTATCCTACACTCAATCTACCTGTGCTGGCTCAGGAC
 CGTGGGGTGCAGCACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCTGGTGCCTGTGGAACAGCGGGCGCTGCCTCAGCTGCAGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTCGGATGCCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCACGTCTCTTTTTCAGCTTCTTGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAGAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCCCTTGAGATGATTTTCTCTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCCTCCCAGCATCTGGGACTCGAGAGTGGCGAGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTCTCTCCACACAGCCTCTCTCCACATCCCCAGCTG
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACACGGGACCACAGGCCTTAGGGATACAGGGGGTCCC
 CTTCTGTGTACCAACCCCCACCTCCTCCAGGACCACTAGGTGGTGTGGATGTTGTTCTTTGGCCAGCCAA
 GGTTACGGCGATTCTCCCCAGGGATCTTGAAGGACCAAGTGTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCCCTACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCACAGGCA
 AGGATCCTGTGCTGTCTGTTGAGAGCCTGCCACCGTGTCTCGGAGTGTGGGGCAGGCTGAGTGGATAGG
 TGACAGGSCGTGAGCATGGCCCTGGGTGTGTGTGAGCTCAGGCCCTAGGTCGAGCTTGGAGACGGGTGTGTTG
 CGGGGAAGAGGTGTGGCTCAAAGTGTGTGTGTGAGGGGCTGGGTGTGTAGCCTGGGTAGGGGAAAGTGTG
 TGCGGCTGCTGTGTGGCATGTGAGATGAGTGACTGCCGCTGAATGTGTCCACAGTTGAGAGGTTTGGAGCAGGAT
 GAGGGAATCCTGTACCATCAATATCACTTGTGGAGCGCCAGCTCTGCCAAGAGCCACCTGGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCTGTGTGCAATGTCCCTCTGTGTGCCCTTTCGCCGCTCTGCAAC
 CTCACAGGCTCCCCACACAACAGTGCCTTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGAAAATGGGGTGGC
 TGGGCTCTCCCATCTCTTTTCTCCTTGCCTTGCATGCTGGCTGGCCTCCCCCTCCAAAACCTTCATTCCCT
 GCTGCGAGCCCTTGGCATAGCTGATTTGGGGAGAGGAAGGGCGATTGAGGGAGAGGGGAGAAAAGCT
 TATGGCTGGGTCTGTTCTTCTCCCTCCAGAGGGCTCTTACTGTTCCAGGGTGGCCCGAGGCGAGGCGGGCC
 ACATATGCTGTGCTTCGGTAAAGGTGACCCCTGCCATTACAGAGCCCTGGCATGTTCTGCGCCACAGG
 AATAGAAATGAGGGAGCTCAGAAACTTCCATCCCAAGGCGAGTCTCCGTGGTTGAAGCAGACTGGATTTTG
 CTCTGCCCTGACCCCTTGTCCCTCTTGAAGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGACTCGGGT
 GCGCTGCGCTAGCTTCTTTGATACTGAAAACCTTTAAGTGGGAGGTGGCAAGGGATGTGCTTAATAAATCAA
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

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FIGURE 217

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGTCCCGTGA
 CTATGGCTCCCCAGAGCCTGCCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
 CTGATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
 CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC
 TGGATGCCGAAGTCTTGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
 CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGCCAAA
 ACTCCAATATGAGGACAAGTTCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAAATTCAAGGAGGGGGCAGAGATG
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGCTCTTCGCCCCATTGA
 GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
 TACGGCTGATCAACAAGTTCAATAGTCCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC
 TTGTATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGT
 TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
 GCCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT
 CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCATGCCCAGCGGCAGTTCTCGAAGC
 TCGGGGGGCTGCAGGTCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
 CGCTGGTCACTGCTCTACGACCTGGTCACGGAGAAGATGTTCCGCCAGGAGGAGGCTGA
 GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
 GCCTGTGGGAACAGGGCTGGTGCGAGATCACGGCCCACTCTCGCGCTGCCCGAGCATGAT
 GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCTCGACCCTGCCGGGACCGCTACCG
 TCAGGACCCCGAGCTCGGCAGGACACTGGCCAGCCTGCAGGTGAGTACCAGGTGCTGGCCA
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCAGGAGCTGCTGGGCTCTGTCAAC
 AGCTTGCTGAAGGAGCTGAGATTGAGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
 GGCTGAGGGGTGCCAGCTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGCCAGTGCTGGCT
 TGCCATTAAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

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FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEDEL
 DAEVLEVFHPTHEWQALPQGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGEVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

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FIGURE 219

TTCGGCTTCCTAGAGGAAGTGGCGCGGACCTTCATTGGGGGTTTCGGTTCCCCCCCCCTCC
 CTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGGTTGCCACCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCAATTGGCTGTCTGGTCAAGCCCCCACCCTCC
 TTCCCACCTGACCGCCATGGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGGTTCCGG
 CCGGCCCTTCGCGCTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTGGT
 CGCAGGGGCAATTTTCTGGCTGGTCTCCCTGTCTCTGGCTCTGTGGTCTGGTTCATCTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCTC
 ATGTTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACTTTGGGCCAGGTGTGGTGGGATCCATGGAGACTCACCTATTACTTCTGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCCTGGTGGTGGGAGTCACCTACTGACATCG
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC
 TCTGTGTAAGGACTGACTACCTGGACTGATCGCTGACAGATCCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATCTCTGTCTCCTTCTCGTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCCTGGGTTTCAAGCAGTCACTGCTGGTGGGTTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCTGTGTCACTGCTCTGCTCTCAC
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCGAGGCCAGCGCAGGAGGACAGTCCGGTGAT
 GGTGTATCTGCCCCGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTCTCCATCTCCAGTTCTGGACAGTGACAG
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTTCTAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
 AGGCCTGAGGGGGAAACCATTTTTGGTGTGATAAATACCTAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATGGAACCTTCTAACCCTCCTTGGGCTATATTTTCTC
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTCCGTCCTTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAAGTGATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTTAACCT
 CCTTAACCCACAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGTACATCGTAGGGAAGGAGGG
 GAGATTTTTTGTAGTTTTTAATGGGGTGTGGAGGGGGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTCTGCTGAGGTGGAGTGCCCATCCTTTTAAATCAAGGTGATTGTGATTTGACT
 AATAAAAAAGAAATTTGTAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVRFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAIILLHTEWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGCTTGAGTGAGGACGGAAGATCAACCCA
TTTCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTGGGATCCATGGAGAC
TCACCCATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

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GACCGACCCGTTCAGATGCCCGGTTCCAGTACGGCTTCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCATTTCATCCGCCAGATGGCCTATGTTTN
TGGNTTTCCTTCGGTATCATCAGTGGTGTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTGCTGTCTGGTCAGGCCCCACCCCTTCCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

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FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCCNTTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCATTGCGCTGTCTGGTCAGGCCCCCACCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTCGGGCCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGCTCTGTG
CTTCTACAGGAGGTGTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

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FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGCTGTGCGTCTGACACCCACATCTTTCTGTGTCCCTCCTTGCCCTGTCTGGAGGCTGT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CTTGTGGTTCTCTCTACCTGGGGAATAAGGTGCAGCGGCCATGGCTCACGAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGCTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATAACTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT
 CAACGCTCCTCTCATTTGTCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGATCCAGGAAACCATCAGGCCAACTCCTTGAGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCCTGG
 GAACAATTTCCAAAAGTTCACAGGGCGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGAAAAA

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FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSSGNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRIPTKDVRPINVSSHCPAGTKCL
VSGWGTTKSPQVHFPKVLQCLNISVLSQKRCEYPRQIDDTMFCAGDKAGRDSCQGDSSGGP
VVCNGSLQGLVSWGDPNRPNGVYTNLCKFTKWIQETIQANS

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FIGURE 227

ATGGTCAACGACCCGGTGGAAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCGCGCGCA
 CAAGCCGACGCGGCGAGCTGCGGCTACGTGCTGTGCACCGTGTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGTGTGTACCGGTGCGGTGCTCTCTGAAACACGACCCACGCGCGGGCAGC
 GCGGCCCCACCTGTCTGTCAGCACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACTCAGCATCTCATTGACCCGGCTGCCCGACCTCACCAGACA
 CTTTGCACGCTGGAGAGCGCCAGGCTCGGTGCTGCAAGGCGCTGACAGAGCACCAGGCG
 CAGCCACGGCTGTGGGCGACAGGAGCAGGAGCTGCTGGACAGCTGACGAGCCAGGCTGCC
 CGGCTGCTGGCCGAGCCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGATG
 GCACGCTGGGCGAGGGCTCAGCGCCCTGCAGAGTGAAGAGGGCGCCCTCATCCAGCTTCTC
 TCTGAGAGCCAGGCGCCACATGGCTCACCTGGTGAACCTCCGTGAGCGACATCTCGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCGGCGCCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGAACCGGGCGGGGCTGTGCCACTGGCTCCGCGGCGCGAGACTGTCTGGACGTCTCT
 CTAAGCGGACAGCAGGACGATGGCGCTCTACTCTGCTTTCCACCCACTACCCGGCGGGCTT
 CCAGGTGTACTGTGACATGGCGACGGACGGCGCGGCTGGACGGTGTTCAGCGCGGGGAGG
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACCGCTACCGAGACGGCTTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCGCTGACCACACAGGCTGCCTACGAGCT
 GCAGCTGGACCTGGAGACTTTGAGAAATGGCACGGCTATGCCGCTACGGGAGCTTCGGCG
 TGCGCTTGTCTTCGGTGAGCCCTGAGGAAGACGGGTACCCGCTCACCTGGCTGACTATTC
 GGCATCGACGGCGACTCCCTCCTGAAGCACAGCGGATGAGGTTCAACCAAGGACCGTGA
 CAGCGACCATTCAGAGAAACCTGTGCGCGCTTCTACCGCGGTGCTGGTGGTACCGCAACT
 GCCACGCTCAACCTCAATGGGAGTACCTGCGCGGTGCCACGCTCTATGCGGACGGC
 GTGGAGTGGTCTCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 GCCGCTCCGGGAGGACCGCT**TAGAC**TGGTGCACCTTGTCTTGGCCCTGGTGGTCCCTGTGCG
 CCATCCCCGAGCCCACTCACTCTTTCGTGAATGTCTCCACCCCACTGTGGCTGGCGGAC
 CCACCTCCAGTAGGGAGGGCGGGGCTCCCTGACACGAAGCTCCCTGGGCGGCTGAAGT
 CACACATCGGCTTCTCGCGCTCCCGACCCCTCAATTGGCAGCTCACTGATCTCTTGCTC
 TGCTGATGGGGCTGGCAAACTTGACGACCCCACTCTGCTGCCCGCACTGTGACTCGG
 TGCTGTTTCCGCTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGCAACCTCTGCCCTGCC
 GCCAAATACCGGCAATTATGGGACAGAGAGCAGGGGCGAGACGACCCCTGGAGTCTCA
 CTAGAGATGTGGGGAATGTCAAGTCTCTCTGAGGTGAGTCTGAGGCGAGTATCTCCAG
 CGCTCCCAATGCGCAACCCCAACCGTTTCCCTGGTGCCCAAGAGAACCCACTTCTCCCCAA
 GGGCTCAGCTGGCTGTGGGCTGGGTGGCCCATCTACAGGCGCTGAGGTGAGGATGGG
 GAGTCTGCTCTTGGGACCAACCGTCTCAAGGCTGAGACCAATCCCTGGAGGCCACCCAC
 CCTGTGCCCCGGCAGGCTGGGGCTGTCAGTCTCTTACCTGCTGTGCCCACTGCTCTCTG
 TCTCAATGAGGCCCAACCCATCCCCACCCAGCTCCCGCGCTGCTCTACCTGGGCGAGC
 CGGGCTGCCATCCCAATTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGGTTTCTGGGCTGGGGCTTAGGCAAGGCTGGGATGAG
 GCTTTGACAAACCCCAACCAATTTCCAGGGACTCCAGGCTCTGAGGCTCTCCAGGAGG
 GCGTTGGGGGCTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGCC
 ATTGACCGTGGCCACCTGGACCCAGGCGAGGCCCGGCGCGGAGTGGTCAAGGGGACAGGA
 CCACCTCACCGGCGAAATGGGGTGGGGGAGTGGGGCACAGAGGAGGCGACCACTGGACA
 TCTTGTTGTTGAATCTCCCAACACCCAGCAGCTGTCTATCCCACTCTTGTGTGCACACA
 CCGTAGGTTGAGACCCGAGGCTCCAGGACCCAGCAGCCCAAGGCGAGGCTGGAGCCGGG
 GCGCTAGCTGTCTGCTCAGGCGCTGGACCCGCGTGGCTTACGTCAGGCCAGATGCAGGG
 CGGCTTTTCAAGGCTCTCTGATGGGGGCTCCGAAAGGCTGGAGTCAGCTTGGGGAGCT
 GCGTAGCAGCTCTCTCTCGGCGAGGAGGAGGAGTGGCTTCTCCAAAGGACCCCGATGGCA
 GGTGCTCAGGGGTGTGGGGTTCCGTTCTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACAATAAATTTGACTTGGCACCCTGGGGGTTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 TGTCCAGTGGCCACAGGTATCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVTGAFLNLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVS DILDALQDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAAYELHVDLED FENG TAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKXSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEM KIRPVREDR

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GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCCTGCTTCCTGAACTAGCTACAGTAGCCCGCGCGCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGATGCAGGCGCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACAGCTCTCCAATACTGGTCAAGACACCATTCTCAAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATTGCTGAAGATAAACAACAAGAGAAGCCTGGAATTTGCCGCTGTCACAGACTCTACTGATTTTTCTACTCTTATTGGACAGGGCTTTTGCGCCCTTGACATGTCGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTCTCGAACTTGTCCATATATAATAGATGTCAACGAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATATCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTCTCTGTGTTTTCTGTTCAGGATACCAGCATTTCTGAGCTTGGGTTTATGCAGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAAATATCACTCCCTGTTTTCATGTCTTCTTACACTTGGTGGAATAAGAACTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACAGCAAATACACAAGGAATTCTTTTTGTTGTTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAAATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCGAGAGAAATATATCCCCATCTCCGTTTTCATATCAGAACTACCGCTCCCGATATTCCTTCAGAGAAATATAAGACAGAAAAAGTGAGCCTCTTCACTGTACCTTGTAAATAGTTTTCAGTTCTATTTTCTTCCATTGACCCATATTTATACGTTTCAGGTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRTEHRAPSSTWRPVALTLLTLCVL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKL
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLE
FAASQSYSEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSRSDCVAILNG
MIFSKDCKELKRCVCERRAGMVKPESLHVPPETLGEGD

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AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTGCGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNCTCTTTTCAACGTGGCGACCAGTGGCCCTGACCCGTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATAAAGCTTGCAAGGAANTGCGCAGCAT
GTGGCTGAAAAACTCTGTGCTGAGCTGTATAACAAGCTGGAGGAACCTTTGAAGAGGAGGCAA
AGTNTCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCGGAGCGCAAGAACCCCTGCGCAGGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCTCCCGGCTCCCGCCCTCGAGACTCCTCTGGCTGCTGCT
 CTGGGGGTTTCGGGGGGGCGGGGACCCGCGCTCGGGGCGCCATGCGGGCATCGCTGCTGCTG
 TCGGTGCTCGGGCCCGCAGGGGCCGCTGGCCGTGGGCATCTCCCTGGGCTTCACCCCTGAGCCT
 GCTCAGCGTCACTGGGTGGAGGAGCCGTGCGGCCACGGCCCGCCCACTCGAGACTCTG
 AGCTGCCGCGCGCGGCAACACCAACGCGGCGCGCCGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGGAGAGAAGCCCGGGGCGGCGAAGGCGCGGGGAGAATTGGGAGCCGCGCTTGGCC
 CTACCACCTGACAGCCCGGCCAGGCCGCCAAAAAGGCCGTGAGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCCTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCAGCGGGCGCGCCGGGCCCACTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTTCTTCTGTTGCTGACACCACTACACCGAGGCGCACGGCTGGCACGCCCTAACTGG
 CCACCTCAGCCTGGCCTCCGCGGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGGGG
 GAGAGCCACCCCGCCGCTACTGCGCACGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG
 CTGCAACAACCTGCGGCCCACTGGAAGGCTGCCGCAACGACATCGTCACTGCGCGCCCTGA
 CGAGTGGCTGGGTGCTGCTCATTTCTCGATGCCACCGGGTGGGCTGCACTGGTGACCAAGG
 GGGTGCACATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGCAGGAGGGACCCCTCAT
 TTCCGAAGTGGCTTGACAGCCCAACCCCTGTGCGTGGACCTGTGCACATGTACCAGCTGCACAA
 AGCTTTGCGCCGAGCTGAATGGAACGCAAGTACCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACAGCCATCTGGCCCTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGAGGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACACCCCGCCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGTACCAGACGCTTTGATCCGGCGCCGGGGTATGGA
 ATACACGCTGGACTTGACGCTGGAGGCACTGACCCCCAGGGAGGCCGCCCGGCCCTTCACT
 GCCGAGTGCAGCTGCTCGGCGCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCAGCTCTACGTGTGCTGCTGCCCTTAGCTGCGGCTGAGCGTGACCTGGCCCTGG
 CTTCTTGGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGACCT
 GTCAAGGCCACGTTGGCAGAGCTGGAGCGCGCTTTCCCGGCTGCCCGGTTGCCATGGCTCAG
 TGTGCGACAGCGCCACCTTCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCCG
 TGGACACATGTTCTGCTGCGCGGGCCAGACACGGTGCTCAGCGCTGACTTCTTGAACCCG
 TGCCGCTGATGCTGCTCTCGGCTGGCAGGCCCTTTTCCCATGCAATTTCCAAGCCTTCA
 CCCAGGTGTGGCCCCACCACAAGGGCTTGGGCCCCAGAGCTTGGGCGGTGACACTGGCCGCT
 TTGATGCCAGGCGAGCCAGCGAGGCCCTGCTTCTACAACCTCCGACTAGCTGGCGAGCCGTGGG
 CGCCTGGCGCAGCCTCAGAACAGAAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGACGCGT
 ACCGGCCAGACGCTGACGCGGAGGCTCAGTGAGGACCTGTACACCCGCTGCCCTCCAGAGC
 GTGCTTGGGGCTCGGCTCCCGAACCCAGCTGGCCATGCTACTTTGAACAGGAGCGAGG
 CAACAGCACTGACCCCACTGTCCCGTGGGCGTGGCATGGCCACACCCCACTCCAGCTT
 CTCCCCAAAACAGAGCCACTGCCAGCCTGCTGGGCGAGGCTGGCCGTAGCCAGACCC
 AAGCTGGCCCACTGCTCCCTCTTGCTCTGTGGGTCCCTGGGCTCTGCACAGCACTGGG
 GGACGTGCCCCAGAGGCCACCACTTCTCATCCCAACCCAGTTTCCCTGCCCTTGACGCT
 GCTGATTTCGGGCTGTGGCCCTCCACGTATTTATGCACTACAGTGTGCCCTGACGCCAGCCCTGC
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTGTGTGGGGAAGGAGGAGCTGAGGAGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCTGCCGAAGCTCCTGCTTTAATAAACTGGCCA
 AGTGTGGA AAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQRLLVAVL
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLLLE
QHGDDEFDWWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGI PAPS RPAS RFVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALT PQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSHLVLRAVEPALLQRYRAQTCSARLSIDL
YHRCLQSVLEGLGSRQTQLAMLLFEQEQQNST

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FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTTCCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCGCCTCATTGGAAGAACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTCATGCGCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACC
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTGA
 ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

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FIGURE 235

MAAGLFGLSARLLAAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPED E

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GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTTGGCGGCAGCGGCAGCGAGGGC
TCCGGGCGCGCCGCTCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGCTCCGCT
GTGGCGGGAAGCGGCCCCAGAACGCACACACGTGGCAAGGAGACCAGAACCCAGGA
CGAAAACCTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

CGCGGGCGCT**TATG**CCGCTTGCTCTGCTCGTCCGGTTGCTCCTGGGGCCCGCGCGGCTGGTGCCCT
TGCAGAACCCCCACGCGACAGCCTCGGGGAGGAACCTTGTCATACCCCGCTGCCCTTCCGGGG
ACGTAGCCGCCACATTCAGTTCCGACGCGCTGGGATTCCGGAGCTTCAGCGGGAAGGATGT
TCCCATCTACAGGCTCTTTCCCAAAGCCCTTGGGGCAGCTGATCTCAAGTATTCTCTACGGGA
GCTGCACCTGTCTATTACACAAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCTCG
AGGCCCATCTAGGTGCAGAGTGTGGGTCTGGTTTCCAAGACACTGCTACTGATGTGGATAA
TCTTTGGAAGGAGCTCAGTAATGTCTCTCAGGATCTTTCTGCGCCTCTCTCAACTTCATCGA
CTCCACCAACAGCTACCTCCCACTGCTCTCTTCAAACCCCTGGGTCTGGCCAACTGACATGT
ACCATACTTTCTGCGCTATGCTGTGCTCGCGGGGAGGTGGTCTGCACCGAAAACCTCACC
CCCTTGGGAAGAGCTTGTGCCCTGTAGTTTCCAAGCAGGCCTCTGTGTGCTGCTGAGGCGAGA
TCGTTTGAAGCTACACAGGCTACCACCTCCAGCGAGTGCATATCCGCCTGTTTGCAAGAAAT
CACGCTGTACTAGCATCTCTGGGAGCTGAGCGACAGCTGTCACTGTTGATTTGATGCCTTT
ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCCGAACCCCTCAGGA
GCCCTGGCCCCCTGGCTTTCAGAGAGCGAGTCTATGTGGACATCACCACTACAAACCGAGA
ACGAGACATTTAGAGGTGCACCCACCCCGCCACCATACATACAGGAGCTCATCTTAGGCAT
CGGAAGACCTATGCCATCTATGACTTGTCTTGACACCGCATGATCAACAACCTCTCGAAACCT
CAACATCCAGCTCAAGTGAAGAGACACCCCAAGAGAATGAGGCCCCCCCAGTGCCCTTCTGTG
ATGCCCGCGGTACGTAGCTAGTGCTATGGGCTCGAGAAGGGGAGCTGAGCAGCACTGCTGTAC
AACACCCACCCATACCGGGCTTCCCGGCTGCTGCTGCTGGACACCGTACCTCGGTATCTCGGC
GCTGTATGTGCACACCCCTACCATCACTTCCAAGGGCAAGGAGAACAAACCAAGTTTACATCT
ACTACAGCGCTGCCACGAGCGGCTGCAACCCCACTCTGGAGATGCTGATTAGCTGCCG
GCCAATCTAGTCACCAAGGTTTCCATCTAGTTTGAAGCGGGCTGCTGTAAGTGGACCGAGTA
CGATCGGACATCTTAACCATGGCTTCTATGTGACGCCATCTGTCTCAGCGCCCTTGTGCCCA
CATCTGGTAGACCGCAAGGAGTGSACTGTGGAAGAGACTCCCTTTCAACAGCCTGTTCGCC
GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
GACACCGGACTTCAGCATGCCCTACACGTACTGTCCCTACGTGCACTGTGGTGGCCGTGT
GTACAGGCTCTCTTCTACAATCTCTCAACCGCAACCTTCCACATCGAGAGGCCCGCAGGT
GGCTTGGCCAAGCGGTGGCCAACTTATCCGGCGCGCCGAGGTGTGCCCCCACTCT**TGAT**T
TCTGCCCTTCTCCAGCAGCTCAGCTCGGCTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT
TCTGCCACTTGCTCTCTCAGAGTTGGCTTTTGAACCAAGATGCCCTGGACAGGTCAGGCG
CTACAGCTGTGTTTCTCAGTACAGGAGCCACGAGGCAAAATGGGCATTGAAATTTGAATTA
CTTAGAAATTCATTCTCACTCACTGTAGTGCCACCTCTATATTGAGTGTCTCAATGAAGCAA
AGTGTGCGTGGCTGCTGATTGGACAGCAGCAAGAAAAGATTTCATCACCAAGAAAGGTC
GGCTGGCAGCACTGGCCAAAGGTGATGGGGTGTGTCAACAGTGTATCTCACTGTGTAGTGGA
TGGAGTTTACTGTTTGTGAATAAAACCGCTCTTTCCGTGGAAATAAAAAA

MPLALLVLLLLPGGWCIAPPRDSLREELVITPLPSGDVAATFQFRTRWDSSELQREGVSHY
RLFPKALGQLISKYSRLRELHLSFTQGFWRTRYWGPPFLQAPSGAELVWVFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTLSSVVFDAFITG
QGKKDWSLFRMFRTLTPECPLEASESRVYVDITTYNQDNETLEVHPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFHLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPVWYRLRYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLEMLIQLPANS
VTKVISQIFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLNLPTPDFSMYPNVICLTCTVVAVCYGSFYNNLTTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATGATGCTGGGTCCCTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGAAGAGTCACAAAAAG
TCCAGACCCCAGGGACGGTACTTTCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCCTTGATCTTGACTTCCAGCCTCTAGAAGTGTGAAGAAATAATAT
TTGCTGTTTATAATCCAA

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AAACCTCAGCACTTGCCGGAGTGGCTCATTGTAAAGACAAAGGGTGTGCACACTCTGGCCAGG
AAACCTAGCGCGGTGAGACTCCCGAGTGCCTACATCAAGGCCCCAGGACATGCAGAACCTCTCC
TCTAGAAGCCCGACCCACCA**AT**AGGTCCTGCTGTGGAGATGCAGGCACCTAGGCCAAGG
CGTCCAGTGGTCTCCTGCTTCTGGCTGTCTCTTCTTCTCTTCCGCTTGCCCTCTTTTAA
TTAAGGAGCTCTCAAAACCGCTTCCAGGCTCAACGCCACAGACAGACATTAAAGAAAGGCT
CTACAGTCCCTGGCAAAGCCTAAGTCCCGAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
TGCAGAGCCAGGCCGAGAGAAACATGCCCTCAACACACAAACCCAGGCCAAGGCCCAACCC
CCGAGACAGAGAGAAAGGAGGCCAACACAGGCACCGCGGAGAGCAGGACAGGAGTGGCCAC
ACAGCACAGAGGGCAGCATGGGAAGAGCCACAGAAAAGAGAAACCATGGTGAACACACTGT
ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCCAATCATGGAAGAGC
AGGACACAAAGACGACCCAAAGGAATGGGGCCGACACAGGAAGCTGACGGCCTCCAGGACG
GTGTGCAGAGAAGACACCGAGGCAAGGCGGCACACAGCCAGAGCGCTCATTCCCAAAGATCA
GCACAGAATGCTGGCTCCCGACAGGACAGTGTCAACAAGGACGAGACAGAAAGGATGACCA
CAGCAGTCTATCCACCTAAGGAGAGAAGAACCTCAGGCCACCCACCCCTCGCCCTTTCCAG
AGCCCCACGACGACGAGAAACCAAGACTGAGGCGCCCACTTCAAATCTGAGCCTCGGTG
GGATTTTGAGGAAAAATACAGTCTCGAAATAGGAGCCTCTCAGACGACTTGCCTGACTCTG
TTAAGATCAAAAGCTCCAAGTGCCTGTGGCTCGAGAAAGCTCTTCTGCCAACCTCACTCTC
TCTCTGGACTCAGACACTTCAACAGAGTGTAGTGGGACCGCTGGAACATTTGCACACC
CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
TGCCCCAGCAGCAGCTGCTCTCTGGCCAGCTCCCCGCTGGGAGCCTCCGGTGCATCACTGT
CCGCTGGTGGGCAACGGGGGATCTCGAAACACTCCACATGGGCGAGGATAGACAGTCA
CGACTACGTGTTCCGATTGAGCGGAGCTCTCTAATTAAGGCTACGAAACAGGATGTGGGCAAT
GGACATCTTCTACCGCTTTACCGCTTCTCCCTGACCCAGTCACTCTTATATTGGGCAAT
CGGGGTTTCAAGAACGTGGCTCTTGGAAGGACGTCCGCTACTTGCACCTTCTGGGAAGGCAC
CCGGGACTATGATGGCTGGAACAGCTGCTTATGAATACAGCGGTGATGTCAAAAACCTTT
TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
TTGCTGCACCCAGACTTTCTCGATACATAGAAGACAGTTTCTTGAGGCTTGAAGCCCTGGA
TGGTGCCACTGAGGATATACGCCGCCACACTGGGGCCCTCTGTGCTCACTGCTCCCTT
AGCTCTGTGACACCGGTGATGCTTTATGGCTTCACTACTGAGGGCCATGAGCGCTTTTCTGAT
CACTACTATGATACATCATGGAAGCGGCTGATCTTTATACATAACCATGACTTCAAGTGGGA
GAGAGAAGTCTGGAAGCGGCTACAGATGAAGGATATCCGGCTGTACCGAGCTCTGGTCT
CCGGACCTGCCAAAGCCAAAGAACT**GA**ACCGGGGCCAGGGCTGCCATGTGTCTCTGGCTGCTC
CAAGGCACAGGATACAGTGGGAATCTTGAGACTTTGGCCATTTCCCATGGCTCAGACTAA
GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAACTCTCTCAAGAT
GGCAAAATGGCTAATTGGGTTCTGAAGTTCTCTCAGTACATTTGCTGTAGGCTCTGAGGCCAGG
GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCAAACTTCTCGCTGAAAACAACTCTT
CCAGTCCAAAAGCTTCTTGATACAGAAAAAAGCGCTGGATTTACAGAAACATATAGATCTG
GTTTGAATCCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACTTCACTAC
AGATTGCTCAGAAGACTTTCTAGAGTTATCTGATTTAGAAAGGCTCTATACTTGTCTGT
TCTTTAAGCTTTTGAACACTCTAGTGTGTGAGAAAACCTGATAATAACAAATGATTGTT
GCTTATGGAAAGGCAATAAATTTTACAGTGAAGAAAAAATAAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTEINIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDGRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPPFGFMEINYSLVQKVVTFRPPVPPQQLLASLPAGSLRCITCAVVNGGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHDPDL
 RYMKNRFLRSKTLGDAHWRIRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Luminal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

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FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACCTATTT

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FIGURE 244

MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMDK

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FIGURE 245

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCGGACCCCGGGCCGCCAGCCCCACCATGCCACCCGCGGGGTCCGCGGGCCGCCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCCTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGACGCCAGTATACCCATACCCCGAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA
 ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTGACGAGCTGGCAGTAGCCCTCCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAGACAAAA

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FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRGSHWHPGFNCEFFTFC CGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDEKAGPAPPQPGFMYPPSGPAPQYFLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

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FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGCGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCACGGTAGGTAGGCAAGAAAGATGGTGTCTTCTGCCCTCAAATGGTCCCTTGCAACCATG
 TCAATTTCTACTTTCTCACTTGTGGCTCTCTTAACGTGTCCACTCCCTCATGGTGTCAAGAG
 CAGTAGAAGCATCTCCAAACGCTAGTGATGGGACACCATTTCTTGGAAATAAAAATACGACTCT
 CTGAGTAGCTCATCCCGATTCTATTATGATCTCTTGATCCATGCAAACTTTACCACGGTAGCC
 TTCTGGGGAACCCAGAAAGTAGAAATCACAGCCAGTCAAGCCACAGCACCATTCACTCTGCA
 TAGTACCACCTGAGATATCTAGGGCCACCCCTCAGGAAGGAGCTGGAGAGAGGCTATCCGG
 AAGAACCCCTGCAGGTCTTGGAAACCCCCCTCAGGAGCAAAATGCATGCTGGCTCCCGAG
 CCCCTCTTGTGGGCTCCCGTACACAGTTGTCACTATGCTGGCAATCTTTCGGAGAC
 TTTCCACGGATTTTACAAAGACCACTACAGAACCAAGGAAGGGAACTGAGGATACCTAGCAT
 CAACACAATTTGAACCCCTGCAGCTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGTTTCTCAATCAAATTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCAATTTTGATGTCACTGTGA
 AGATAGGACCTATCTGGTGGCCTTCATATTCAGATTTTGAGTCTGTCAAGCAAGATAACC
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCGACAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTCTAGAATTTTATGAGGATTATTTCAAGTACCCGTATCCCC
 TACCCAAACAAGATCTTGTGCTATTCCGACCTTCAGTCTGGTCTATGGAAACTGGGGA
 CTGACAACATATAGAGAATCTGCTCTGTTGTTGATGCAGAAAGTCTTCTGATCACTCAAGTAA
 GCTTGGCATCACAGTCACTGTGGCCATGAACCTGGCCACAGTGGTTGGGAACCTGGTCA
 CTATGAATGGTGAATGATCTTTGGCTAAATGAAGGATTGGCCAAATTTATGGAGTTTGTG
 TCTGTCAGTGTGACCCATGCTGAACCTGAAAGTTGGAGATTATTTTGGCAAAATGTTTGA
 CGCAATGGGAGTAGATGCTTAAATTCCTCACACCCCTGTGTCTACACCTGTGGAAATCCGT
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGAGCTTGTATCTGTAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCAATTTAAAGTGGTATTTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAATACAAAAACGAGGACCTGTGGGATAGTATGCAAGATTTTGGCTACAG
 ATGGTGTAAAGGGATGGATGGCTTTTGTCTAGAAGTCAACATTCATCTTCATCTCACAT
 TGGCATCAGGAAGGGGTGGATGTGAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT
 TCCCCTAATACCCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGGCTCTGACGGGCCCCGGACACTGGGTACCTGTGGCATGTTGCCATTTGACATTCATACC
 AGCAATCCAAATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCC
 AGAAGAGGTGGAATGGAATCAAATTTAATGTGGGCATGAATGGCTATTACATTTGTGATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACAGCAGTCAAGCAT
 AATGATCGGGCAAGTCTCATTAAACAATGCAATTCAGCTCGTCAGCATTTGGGAAGCTGCCAT
 TGAAAGGGCCTGGATTTATCCCTGTACTTGAACATGAAACTGAAATTTAGCCCGTGTGTTT
 AAGGTTTGAATGAGCTGATTTCTATATAGTAAATGGAAGAAAGAGATATGAATGAAGTG
 GAAACTCAATTAAGGCCCTCTCTCATCAGGCTGCTAAGGGACCTCATGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCTCTCGCTGTG
 TGCACAACATACAGCCGTGCGTACAGAGGGCAGAAGGCTATTTGAGAAAGTGGGAAGGAATCC
 AATGGAACTTTGAGCCTGCCCTGTGCAGTGAACCTTGGCAGTGTGTTGCTGTGGGGGCCAGAG
 CACAGAGGCTGGGATTTTCTTTATAGTAAATCATGTTTCTTTGTCCAGTACTGAGAAAAA
 GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAATTAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAAACTCAGGAGTTTCCACAAATCTTACACTCAATTGG
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAACTGGAAACAACTTG
 TACAAAGTTTGAATTTGGCTCATCTTCCATAGCCACATGGTAAATGGGTACAAACAAATCAA
 TTCTCCACAGAAACACGGCTTGAAGAGTAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCCGTTGTGCTCAACAGACAAATGAAACCATTTGAAGAAAAATCCGTTGGATGG
 ATAAGAAATTTGATAAAATCAGAGTGTGGCTGCAAAATGAAAAGCTTGAACGTATGTA
 TTCTCCCTTGGCCGGTTCTCTGTTATCTCTAATCACCACAAATTTTGTGAGTGTATTTTCAA
 ACTAGAGATGGCTTTTGGCTCCAATCGGAGATCTTTTCCCTTCACTTCACTTATTTTGA
 CTATCCCTGTGAAAGAAATAGCTGTAGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA
 TCGCTACCATGTGTTTGTGTTCTCATCAGGTGTTGCCCTGCAACGTAAACCCAGATGTTGGGT
 TCCCTGCCACAGAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPCFDEPAFKASFSEIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVKITKSGVKVSVYAVDPKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELHQWFGNLVTMEWWNDL
 WLNIEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHYSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKMTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYIIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLEKMRDMNEVETQKFAFLIRLLRDLIDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
 RTQNKEKLQWLLDESFKGDKIKTQEFQILTLIGRNPVGYPYLAQWFLRKNWNKLQVQFELGS
 SSIAHVMVGTNTQFSTRLEEVKGFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

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FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCGCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGACCACCATTTATGACACACGAAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTGCTGGGCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGCGCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCTTCTGCTAACTCTATTACCCCCACGATTCTTACCAGTGTCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCACACACAATCATTATCTACTACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 250

MSAVLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

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FIGURE 251

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCGCT
 CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTCTGCTACTGCTG
 CCATCTGGACATCTCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCCCCCCGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGACAGCTGAGCATGCCCAAGGACAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATG**TGA**CGCTCAGGCTGGGGCTGCCCATTTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAACTGAGAAAAATGGCCTATGCTTAAGAGGAAAAATG
 AAAGTGTTCCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFINKAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

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FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
 AA

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FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGTCTACCGCTGTCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCGGTGGTGTGCATCCCCTTGGGGC
 TGCTGTTCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGCTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCGAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCCGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCCCTGTCTGGCTCTGGCTCTGTTCTTAACATCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGAGTCCCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTGCAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGTGCTACTTGACCCCAAGCTCCAGTG
 TGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGAGCCTCCACCTTGGCCATCCGTGAGTATGAATGGCTT
 TTTAAACAAACCCACGTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAA

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FIGURE 256

MSCVLGGVIFLGLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

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FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**TAT**GGG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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FIGURE 258

MGSGPLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

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FIGURE 259

AATTGTATCTGTGAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAGAAGCTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATCTGTTTCTGATGTGGGGTTCCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCTCC
CTCCGATTGTTCTAAAT**TAA**ATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTGTGAATAGCCTTTGAAATTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAAGGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTTCTTGCAGCTTTTCTGCCCGCGCAGTGATC
 CCAGGCCCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGCTTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAAGCAACGAGGGCATACATTCAAGAATTCGAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTACAGCTACACAAGTGAGTACAAGAGTGCAAGTGGGTAACTT
 GGCAGCTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACTGGCAGAAATGTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTTATTAATTGGATCCGAGAACCAACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTCTATGGAGGATTAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTCTATAACCAAGCAACTT
 CTAAATGAGATAATCAAATATAACCTGCAGAAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCTATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTGCTCTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTGTC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCCCAGAGAT
 AAGCAGCTCTATGCTTGAATGAAGGAACAGATCATTTACAAACTCCAGACAAAGAGAAA
 GCTGCCCTGGAAGTAAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCTCTTTCCCAAATGTCACTGCGCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACATGTCCATTACTCCCCCAA
 CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGGTTTACT
 GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCAACTAAAATACATAATATTCTTTT
 CTTTTCTTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATAGTATTTCTTATTGAGGTTTAACTCTATTCCCTAGCCCTGTC
 CTTCCTTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTGTGCACATCATTTGAATTTCTCGTTTCACTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCACTTCTAGAGTTTGGGTGAGTAACACAATTACAAGTGAAAGATACAGC
 TAGAAAATACTACAATCCCATAGTTTTCATTTGCCCAAGGAAGCATCAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCAATGAGCCTTCAAAATGATAATTCCTCC
 TTTAGCCAGTTTTCATGCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCC
 AGAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTGCTGCTGCT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

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FIGURE 262

MMVALRGASALLVFLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRARIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLNASCNMLMGIKSLKIVKKMMDTHGSGMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPFRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 263

GGGGCCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**AT**GGAGCTCTCGCAGA
 TGTGCGGAGCTCATGGGGCTGTCCGGTGTGCTTGGGCTGTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGCGGCGCGCCCGCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTC
 GGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCTGGCTGCAGCTCTGAGAGGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCTGACGCGAGAGCACCAGCA
 TGAGAGCCAACTGGAGCTGGACCACGCCACCTGGTGGCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAAGCGCCTGTCA
 TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTCT
 CTCATCTGGAGCCCTGAAGGGTCAAGTGCTGTCTTACCATCAACACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAA
 CTAAAGGGCCACTCCGCGGCTGTGCACTCGTTTGTCTTCCACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGTGGAATACAGAAGAAGC
 AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGGGGTGCCGCGCCGTGGCCG
 CTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTATCTCTTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCTCTGTGGGACCGGGCGGTGCGGCTG
 TTTCACAACACTCTTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTTGA
 AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCCTCCTCATGGCACTGTGCCATCTTTCCTCCAGGTGGAAGCCCTTCAGAAGG
 AGTCTCTGGTCTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTCT
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTTGGCCCTTGTGGCAGCACATCCTCACACCCCAAAGAAG
 TTTGTAAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTGTCAAGGA
 TGGGAGACTGGGATAGCTTCCATCACAGAACTGTGTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCCCTCAGTTCATTTGTAAGATGGAGAATAAATCCTCTCTGTGAACCTCTTGA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAAGTAGAAAAAGT
 AGTACTATTGTCCAATGTCATGAAAGTGTAAGTGGGAACCACTGTGCTTTGAAACCAA
 TTAGAAACACATTCTTGGGAAGGCCAAGTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTGGGAGATGATATCTGTTTAAAGGAGACCTCTTTTCAGTTTCATCAAG
 TTCATCAGATATTGAGTGCCCACTCTGTGCCAAATAAATATGAGCTGGGGATTAACAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGILLALMATAAVARGWLRAGEERSGRFACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPPQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVFKMTKREDGGYTFATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLLKRASNESTRQLQQQLTQ
AQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTTGCCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCTAGTAAGTGTGTCTGACTGTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCGCT
 GGGGCGGGAAGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGTGTTGCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGCCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGTTCTCTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCTCCCTCCCTCCCGAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCACT
 TAACCACTGAAGCCCCAATTCCCACAGCTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCA
 AGGATCAGCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFDPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

0000732-11101

FIGURE 267

AGCGCCCCGGCGTCGGGGCGGTAAAGGCCGGCAGAAGGGAGGCACCTTGAGAAATGCTCTTTC
 CTCCAGGACCCAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCTTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAGGCGGAAGAT
 GATGTTTATGGGATTATCCGTCTGGGAGTGTGGTACAACCTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGATT
 GTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 CTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

0008732.11101

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCCCTGGCCGAGATGCGGTAGGAGGGGCGAGCGCAGAG
AGCCCCCTCCTCGGCGCTGCCAACC CGCACCCAGCCCATGGGGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAAGGCTGCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCATAATTGGACT
TTATTAATTTTTAAAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

09989732.111901

FIGURE 273

GCCAGGAATAACTAGAGAGGAAACA**ATG**GGGTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCCTGCTGCACCAGTCAAATCACTTCCCTTCATTAAAGCTGAATAAATAGGCTTTGAAGATA
 TTGCTATTGTTATAGATCTCTACTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTTTTGCAAGCCACAGAAAAAGATTTTTTTCAAAAA
 TGTATCTATATTAATTCTCTGAGAATTGGAAGGAAAAATCTCAGTACAAAGGCCAAACATG
 AAAACCTATAACATGCTGATGTATAGTTGCACCACCTACACTCCGAGGTAGAGATGAACCA
 TACACCAGAGCAGTTACAGAAATCTGGAGAGAAAGCCGAATACATTCACTTCCACCTGACCT
 TCTACTTGGAAAAAACAAATCAATATGACCAACCAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCCGTGGGGAGTGTTCATGAGTACAATGAAGATCAGCCTTCTACCGTGCCTAAG
 TCAAAAAATCTGAGGACAAAGGCTTCCGACAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCGAGCTGTCTTACTAGACATGCAGAATTGATCTACACAAAACTGTATG
 GAAAAGATTGTCAATTCTTCTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCTGTTCGTAATTTTGTAAACGAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAAACATAAAGTGCAAATTTAGAGATACATGGGAGGTGATTAGCAATCTGAGGATT
 TTTAAAAACACATACCCATCGGACACCACTCTCCACCTGTCTTCTCATTTGCTGAAGATC
 AGTCAAGAATTTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAGGACCGCCT
 AAATCGAATGAATCAAGCAGCAAAACATTCCTCTGCAGACTGTTGAAATGGATCCTGGG
 TGGGGATGGTTACATTTGATAGTACTGACCACTATTGTAATTAAGCTTAATCCAAATAAAAGC
 AGTGATGAAGAAACACACTCTGAGCAGGATTACTACATATCTCTGGGAGGAACTTCCAT
 CTGCTCTGGAAATTAATATGCAATTTCCAGGTGATTGGAGAGCTACATTTCCAACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTG
 AAACAAAGTACGGGCACTGTCTCAATTTTATGCTTTGGGAAGAGCTCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATTAACAGGAGGAAGTCAATTTTATGTTTCAGATGAAGCTCAGAACTATG
 GCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAGTCCCTT
 CAGCTCGAAATGAAGGAATTAACACTGAATAGTAATGCTGGATGAACGACACTGTCAAT
 TGATAGTACAGTGGGAAGGACACGTTCTTTCTCATCATGGAACAGTCTGCCCTCCAGTA
 TTTTCTCTCTGGATCCAGTGGRAACAATAATGAAAAATTTACAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCCAGGAACCTGCAAGGTGGGCACTTGGGCATACAATCTTCAAGC
 CAAAGAAACCCAGAAACATTAACATTAACAGTAACTTCTCGAGCAGCAATTTCTTCTGTG
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCAGGCCCAATGATT
 GTTTTACCGAGAAATTTTACAAGGATATGTACCTGTCTTGGAGCCAAATGTGACTGCTTTTAT
 TGAATCAGAGATGGACATACAGAAATTTTGGAACTTTTGGATAATGGTGACGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAATGGCAGATAT
 AGCTTAAAGATTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTTACGGCCTCCACT
 GAATAGAGCCGCTGATACACAGGCTGGGTAGTGAACGGGAAATTTGAAGCAAAACCCGCCAA
 GACCTGAAATTTGATGAGGATACTCAGACACCTTTGGAGGATTTCAAGCCGAACGATCCGGGA
 GTGCAATTTTGGGTATCCAAGTCCCAAGCCTTCCCTTGCCGTGACCAATACCCACCAAGTCA
 AATCACAGACCTTGATGCCAAGCTTCACTGAGGATAAGATTATCTTACATGGACGACCCAG
 GAGATAATTTTGTATTTGAAAAAGTTCAACGTTATATCATAAGAAATTAAGTCAAGTATTCTT
 GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACCAAGGA
 GGCCAACTCCAAGGAAAGTTTGCAATTTAAACCAGAAAAATCTCAGAAAGAAATGCAACCC
 ACATATTTATTTGCCATTAAGAACTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACAT
 GCACAAGTAACTTTGTTTTCCTTCCCTCAAGCAATCTGATGACATTGATCTACACCTATCTC
 TACTCTTACTCTTACTCTGATAAAAGTCATAATCTGGAGTTAATATTTCTACGCTGGTAT
 TGTCGTGATTTGGGTCTGTTAATTTGTTAACTTTATTTAAGTACCACTTTGAACCTTTA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAGT
 AAAGGATATTTCTGAATCTTAAATTTCAATCCCTGTGTGATCATAACTCATAAAAATTAAT
 TTAAGATGTCGGAAGAGGATACTTTGATTAATAAAACACTCATGGATATGTAAGAACTGT
 CAAGATTAATTTAATAGTTTCAATTTTGTATTTTATTTGTAAGAAATAGTGATGAAC
 AAAGATCCCTTTTCACTACGTACCTGGTTGTATATTTATTTGATGCAACAGTTTCTGAAAT
 GATATTTCAAAATGCAATCAAGAAATTAATATCATCTGAGTAGTCAAATACAGATAAA
 GGAGAGCAAAATAAACACATTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFKNVSLIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCQGGGCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSDFKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRLLNRMNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGDNNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQDGVYSRYFTAYTENGRYSLKVRAGH
 GANTARLKLRLPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFDVGKQVRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCAGGAAAGACCATACGTCCCCG
 GGCAGGGGTGACAAAGGTGTCTATCTTTTGTATCTCGTGTGTGGCTGCCCTTCTATTTTCAAGGAAG
 AGCCAAAGTAATTTTGAACCCAGAGGAGCAATGATGTAGCCACTTCTTAACCTTCCCTTCTTGAACC
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCACTCAACCCAGCAAGCGGCTCCTTCGGCTTAACTT
 GTGGTTGGAGCAGATACCTTTTGGGGCTCGCTTCTTAGCAGTGTCTCAGAAGTCACTTGTCTGA
 GGGTGGACAGAGAAAGGAAGGTCCCTCTTGTCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
 AATGAAGTGAATACTTGGAGATTTCACTTCACTATGCTTCTCGCTGCAAGATCATCTCTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAGAGGCGAGAAGCTGTTCTAGAGAAGAAATGGAT
 CAAGCAGCTCCGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCGGTGGGG
 GCGCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCTAGGCTGATTTCTGAATGATGATGGTTCGG
 GGGGGCTGCTTGGCGTGAATTTCCCGGGTGGTGGTTTGTGGTGTCTCTGTGTGCTATCTCTGT
 CCTGTACATGTTTGGGCTGCACCCCAAAGGTTGACGAGGAGCAGCTGGCCTTCCGCAAGGCAACAGC
 CCCAGCGGGGAAGGAGGGGTACCAGGCGCTCTCTCAGGAGTGGGAGGAGCCAGCCCACTACGTGA
 CGAGCTGAAGCGGAGATGCGACAGCTCAAGGAGAGGCTGCAGGAGAGGATGAGCAAGCTCAGGAA
 TGGGCAATACCAAGCCAGCATGCTGCTGGCTGGGCTTGACAGGAGGCCCCAGAGAAACCCAG
 GCCAGCTTCTGGGCTTCTGCACTCGCAGGTGGACAAGGAGGTAAGTGTGGCGTCAAGCTGG
 CCACAGAGATGACGAGCTGCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
 CCTTACCCTGCCACCCCGAGGAAGCCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGGAAGCCATT
 GAATAGCCCTTGGAGACCTTGAAACATCTCGACAGAAACAGCCCAATCACCGCTTACACGGCCT
 CTGATTCGAAAGGGATCTACCGAACAAGGGACAAGGGACATTTGATGAGCTCACCTTTCAA
 AGGGGACCAACAAACAGCAATTCAAACGGCTCATCTTATTTTCGACCATTCAGCCCAATGTGAAGGT
 AAAAAATGAAGGCTCAACATGGCCAAACAGCTTATCAATGTTATCGTGGCTCTAGCAAAAGGGTGG
 ACAAGTTTCCGGGAGCTTATCGAGAAATTTACGGGAGAGTGTGCAATGAGCAGGATGGGAGAGTCTCATCT
 CACTGTGTTTACTTTTGGGAAGAAGAAATAAATGAAGTCAAGGAAATCTTGGGAACCTTCAA
 GCTGCCAATCTCAGGAACCTTTACTTCAATCAGCTGAATGAGAAATTTCTCGGGGAAGGAGCTTG
 ATGTTGGAGCCCGCTCTCGAAGGGAACAGCTCTCTCTTTTCTGTGATGTGACATCTACTT
 CACATCGAATTCCTCAATAGCTTAGGCTGAATACAGCAGCGAGGAAGGATTTTTCAGCTT
 CTTTTCGACGATCAATCTCTGGCATAATATACGGCCACCATGATGAGTCCCTCTTGGACAGC
 AGCTGCTATGGAAGGAAGAACTGGATTTTGGAGAGACTTTGATTTGGGATGACGTTGCAGTATCG
 GTGACACTTTCATCAATATAGTGGGTTTGTATCTGACATCAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGAAGTATCTCCACAGCAACCTCATAGTGGTACGAGCGCTTTCGAGGAGCTTCCAC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTCAAGATGTGCATGCACTCAA
 GGCCATGAACGAGGACCTCCACGGCCAGCTGGGATGCTGGTGTTCAGGACGAGATAGAGGCTCAC
 CTTTCGCAACAGAAAGCAAGACAGTATGCAAAAAAATCAAGTACTCCACAGAGAGGATTTGGGGAGA
 CACTTTTCTTTCTTTCTTTCGAATTTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGGAGC
 ACAAAAAGAAATGGAGTGTGGGTCAGAGATGAGAAGGCTCCGATTTCTCTCTGTGGGCTTTTAC
 AACAGAAATCAAAATCTCCGCTTTGGCTGCAAAAGTAAACCGATTTCTCTGTGGGCTTTTAC
 AAGGCGAATGCTTGTGATTTAAGCCTAATGCTGTGAGGTTTTCAGCTTGTGAACTTGTGACAT
 GAGACCTGTTTGTGCTGCTCAATTGAAATATCATGATTTAAGACAGTTTTGTAAAAAATTCAT
 TAGCATGAAGGCAAGCATATTTCTCTCATATGAATGAGCCTATCAGCAGCTCTAGTTTCTTAGG
 AATGCTAAAAATATCAGAAGGCAGGAGAGAGATAGGCTTATATGATACTAGTGAATACATTAACTA
 AATAAAATGAAAGAAAGAAAGAAACCATAAATCTGTGTATATTTTCCCAAGATTAACCA
 AAAATATCTGCTTATCTTTTGGTGTCTTTTAACTGTCTCCGTTTTTTTCTTTTATTTAAAAAT
 GCACTTTTTCCTTTGGTGTGATGTATAGTCTGCTTATTTAATACCATTTTCGAGGCTTACAGAGA
 GCACAAGTTGGCTCAATTTTTATTTTTAAGAAGATCAATTTGAGATGCTTATGAGAACCTTTCA
 GTTCAAGCATCAAAATGTATGCCATATCCAAGGACATGCCAAATCTGTGATCTGTGAGGCACTGAAT
 GTCCAGCATTGAGACATAGGGAAGGAATGGTTGTACTAATACAGAGCTACAGATCTTCTCTGAA
 GAGTATTTTTCGAAGGCAACTGAACCTGGAGGAAGAAAGTGAACATTTCTGCTTTCAGGAA
 AAGGAACATCTACAGCTGGTATATCTGATGTACCTAAAGTCAACATTTCTGCTTTCAGGAA
 GAATGAGGACCGCTTCTTACCTTTTAAATAAACCAAGTATACCTGTGAGAACCAATATATAT
 TTTCAAAACAGGCTGCTCTCTGCTTCTGGCTTCCATAAGAAGAAATGGAACAAATATATATAT
 ATATATATATTTGTGAAGAGTCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTGTGCTACAT
 GTTATCCACCCAGGCGAGGTGGAAGTAAGTGAATTTTAAATTAAGCAGTCTACTATCA
 CCAAGATGCTTGTGAAATTTGATTTTATACCATTTCAAACATTTTTTAAAAAATAATACAGTTA
 ACATAGAGTGGTTTCTTCACTATGTGAAATTTATAGCCAGCAGGACATGCTAGAGCTAATATCT
 CTTTGTAGTCTGCTTCTGTTTGTCTACAGTAACTCATTTTAAAGCTTCAAGAACCTTCAAGC
 TGTGGTGTGTTAAAAAATGCATGTATTGATTGTACTGTGATTTTGAATTTTAAATTAACCAAC
 AGGCCATGAATGGAAGGTGGTATTCACAGCTAATAAAATATGATTTGTGGATATGAA

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FIGURE 276

MMVVRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVVKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNKELNMANTLINVIVPLAKRVDFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKCMQMS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

000072-11901

GAAAGA**ATG**TTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCACTGCTGAACCTCTGTCAACC
AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT
ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTCTGCTGTTGAGGTGC
AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTCTTTCTAAATGACCAAACCT
CTGGAATTTTTAAAAATCCCTTCCCACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCAC**TACT**GATTTTAT
CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
AAGTGTGAAACATGATCACAAATGAAAAATGGCATCCCTCTGATCCCTGGACATGAAGGG
GGGCATATTAATGATGCCTTCA**TGA**CAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
TGTTCTGCCTCTCTCAAGAAATAAACATTTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
CCAAGAGCAGATCATATATTTTGTTCACCAATCTCTCTTTTGTAATAAAATTTTGAATGTGCT
TGAAAGTGAAAGGAATCAATTATATCCCAACCAACCACTGAAATCATAAGCTATTACAGAC
TCAAAATATTTCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
TAGTTATTGATTTAAGCATTTTTAGAAAATAAGATCAGGCATATGTATATATTTTACACTTC
AAAGACCTAAGGAAAAATAAATTTTCAGTGAGAAATACATATAATATGGTGTAGAAATCAT
TGAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
TGAGAAGTAATTATTGTAATGGATGGATAAAAAATGGAATTACATATACAGGGTGGAAAT
TTATCTCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTAATAGGAC
AATTCATATTGTTGACCAATTTCTACAAATTTGAAAGTCCAATCTGTGCTAACTTAATAAAG
TAATATATCATCTCTTTTTTAAAAA

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FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQMLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRKKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

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FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGT
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACCTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTTAGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTATTAGAAGACACAGACTAACAATTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGAAAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCCCTTTCAGTATTTCTTTAGCAGCATTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCCTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATCAAACCTGTTAAATGACATTTTTATTTTATGTCTC
 TCCTTAACATATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
 TTTGTGC

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVI GEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNQEKVSVYLEDTD

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GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTACCACCATGAAGTTCTTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAAAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTGTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCTACCACTGCAACCACCGCTGCTTCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGTTGGGGATCTCCCGAATGGTAGAGTGTGCTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTATGCTTCCTGTGATTTT
ATCCAACTACTTACCTTGCTACGATATCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGCCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAAACCACAGGCTGG
 ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTA~~AA~~AACTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAACATGGTGAAACCTTGCTCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
 GCAGGAAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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FIGURE 285

GTCA**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCACGCC**TGA**ATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGAGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTELLGQEVSRGRDAAQELRASLLETQMEEDIILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQLRLHTAALPA

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FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGCATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCGATTAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACGTGTCTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAAAT**TAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTCAATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAGAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATTAACCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGCTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACCATTCGATTACAACCTCTAACTTAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATATATGTTTAAAGTCTATATGAGGCAACCAATCTT
 TGGAAAGCTGAAAACGAATTTAAGAATGCTATCTTGGAATTTGCATACGTCTGTGCAATT
 TTTTATTTCTGCCTAGTGCTATTCTGCTTGTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAGTTTAGACTTGAGGGGAAATGGGCTTTTGAAGCAAAACAATTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTAACTACACATGCTTGGAATTAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRS LPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCCGAGGTTCCCCGCGCGC
CCCCAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CAGCCGCGAGGGCTGAAAACCCCGCCGGGGAGGACCGTCCATCCCCTTCCCCGGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAPVAPVALESAAEAGAGTLANPLGTINPLKLLLS
SLGIPVNHIEGSQKCVaelGFPQAVGAVKALKALLGALTVEG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAAGTCTCCTGCTCTCCGTCCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAAGAGAAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCCAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCCACCAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCCAACCTGGAACT
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGACCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGAAAAATCCCAAACCT
 GTTTGATGAGATTAATCTGAAACCAAATTAATTTCTGTGGATTACATCTTGTTCRAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTCACCGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAAGTGCCCATGATGTACGGTGCAGGCAGGTTTGCCCTCCACCTTTGACAAGAA
 TTTTCGTTGTCATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAACTCTCTCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCAGTGAAGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTTCCATGCCTCCTGTATCAAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTA**TAA**TTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTGTCTTAACTAGTTTAGGTTGTCTC
 AAATAAATACAGTAGTCCCACTTATCTGAGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTTGGCAGGGGAGAAATCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC
 TGCTTAAAGACTTTTAGATTGTTTATTCTGGAATTTTCACTTAAATGTTTTTGACCATGGT
 TGACCATGGTTAACTGAGACTCGAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAA
 GCATTAATGATACATATTTTTTAAAAA

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FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
TGTTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

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FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAKVPKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPCLLTTEKPRGQGRGFILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCCTGC
 TGTTTTCTCATAGCGACCACAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGCGCATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCAGTG
 CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAAAGCATCTTATTACTCACCCATGGCCAGCGGGAATTCAGTGCGGGATT
 TGTTCAGTTCAAGGTATTTAATAACGAGAGAGAGCCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCACAGAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVIPVVYDFGDAQKTASYYSPTYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCTGCCCTCGGAACAATGGGGACTCGGCGCGCAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTCT
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATTCT
 CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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FIGURE 298

MGLGARGAWAALLLGLTLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

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CAGCGGGTCCCAAGCTGTGCTTGAGCTTGAGCTTGAGCTTGAGCCGAGCCGGAGCCGG
TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGGACCTGTGGGGAGGC
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCTGCTGCGCTTCCGTGCTGCTGCTGGC
GCAGCTGTGACAGCGCCCAAGAATTCGAGGATGTGAGATGTAATGTATCTGCCCTCCCT
ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCTT
CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAAAGTGCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTGTGCTTTGGACCG
CATGTTGTCTCAGCTTAATTTGGGAATTGAATTCGAAGTGAGTAGAAGAAAGACGACAGACA
CTGGAAGAACTGACTGGGTTTGGCTGGGTTTCATTTTAACTCTTGTGATTTTACCAACT
GTTGCTGGAAGATTCAAACCTGGAAGCAAAACTTGTCTGATTTTTTTTTCTTGTAAACGTA
ATAATAGACATTTTAAAAAGCACACAGCTCAAAGTCAGCCAATAAGACTCTTTCTATTTG
TGACTTTTACTAATAAAATAAATCTGCCTGTAAATATCTTGAAGTCCTTACCTGGAACA
AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTACGGGTTTTTG
TTGTTGTTGTTTTTTGTTTGTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAAATAGACCTTACCTTCTATTG
TCGAGTTTCACTTTATATTTTGAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
ACTTTTGCACGTACTGTATTATCTGGGTATCTGCTGTGCTGCACCTTCATGGTAAACGGGAT
CTAAATAGCTGTTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGCTGTGAT
CAATGCATCTAGAACAACTGGCCATTGTCTAGTTTACTCTAAGACTAAACATAGTCTTG
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGACAATCCTAAGGACTTGGACACT
TGCAATAAAGAAATTTGTTTAAACCCAGCCTCCCTGGATTGATAATATACACATTTG
TCAGCATTTCCGGTCTGTGTTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAGT
AGGGCTGGGGTGTGGGTGCCTCTCTGAAAGGTCTAACCATTTATTGGATAACTGGCTTTTT
TCTTCTATGTCTCTTTTGAATGTAACAATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII IYLSILGLLLLYMVYLT
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVLS

0989732.11301

FIGURE 301

GCACCTGCGACCACCGTGAGCAGT**CATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGCTCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAAT**TGA**AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTACAACTAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

0000732-11-0000

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI
ILHQ

09989732.111901

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGGCAATTGCCTCCCCTGGGTGCTCTTCATCTT
GGATTTGAAAGTTGAGAGCAGCAGTGTGTTTCCCCTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCTGAGCTAACAGTCCATGTG
GGTGATTGAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGCAAATGTATATTCAGAT
AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTCCAGAACCCGCTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGATGGGATGTGTTTCCAG
AGCACAGAAGTGAACACGTCACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAAGGA
GGAGATTGATTTTCGTTACTACCACAACTCAGGATGTCTGGGAGTACTCCGAGCACTGGG
GCCATTCTCGAATCGTGTGAACCTGGTGGGGACATTTTCGCAATGACCGGTTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGCTCTGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGCCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTCAGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCTGTGTGTGTCCTGGGCCACTCTACAGTGATTTGAGACTCCCGCTCTC
CCAGCTGTCTCTGTCTCATTTGTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTGGC
TCTTGAGATGGGACAGCTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCTCAAACCCCTGTT
GGTAGACACCTCTGTGGGCGAGGGTTCTTAGTGAGATGAGTTACTGGGAAGCAATCAGAGATA
AAAACCAACCAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTYICEIRLKGES
QVFKKAVVLHVLPPEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKKTGKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWP SLR
SDRNN SLEKKSGGGMPKTQQAF

099073.11004

FIGURE 305

CTATGAAGAAGCTTCCTGAAAAACAATAAGCAAAGGAAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATGTAAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**
GGATGAAGATGGATACATCACCTTAAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTGAGTTTTTGGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

0960732.44001

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

0909732.111001

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCCGCGATCCCCGG
 CCCGGGGCTGTGGCGTTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGACCCG
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
 GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGCACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGCAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGCGCGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCA
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCAGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
 GTAGCCAGTGAGGGCAAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCTTCAACCAAAAGTTCAAATTTGTAGTGACATTTACCAACAACACAGG
 CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

0959732.11001
 105117.2526960

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELTPECKFKESVVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

0000732-11001

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTGGGGGGATTTTCAGTGAAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCTGACATTGCGAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGAATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCCTTGGAATTTAGTGGGCTCTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGTTAACTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCTGCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGG
 CGCAGCGGCGCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCAACCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTCTACCGCCAGCGTCGTTCTGCGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVS AQRRVCPRGTKSLCQQLLLLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLAQNPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

000073.11001

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCAAGTCAACAAGAGTAAGACAACATAG

0000732-14001

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDSPASRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLLQMPDGDALDGTCKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

000077.11.0000

FIGURE 313

GGGGAGAGGAATTGACCATTGAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAGAGACGAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAATGTGTATATGTGCACACAGGAGAGCAATCAAGAAATG
 AAATAAACAGAGTTAGACCCCGGGGGTGGTGTCTGACATAAAATAATATCTTAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGAGTTACAAAGAAAAAGTATGTTCAATTT
 TTCCTATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTTGGAATGAAAGTTTGGGGCTTTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTCAGAGAAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCGAGAGCA
 CAGTTGGATTGTGCCTATGTTGACTAAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATTCTTTTGGTATCAAGATCATCGCTTTTCTTGTCTTAAACCCTGGATTTCCATCT
 GGATGTTGCTGGTATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACAGGATAAAATGATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTGCTGCTCTTCAACTTCTTGTGGTGGTGGTGGTGGTGGGGCTCAGACCTGCCCTTCTGTGT
 GCTCCTGCAGCAACAGTTGAGCAAGGTGATTTGTGTCGGAACCACTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCATTGAG
 GCATTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTTGATACCTTGTCTAAA
 CTGAAGAGCTCTGGTTGCGAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT
 CGCCGCTAGACTTAGGGGAATGAAAGACTTTCATACATCTCAGAAGTGCCTTTGAAGTCTGTCCCACT
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACGCTCATAAAACTAGATGAG
 CTGGATCTTCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTCCAGGCTTGATGCACCTTCAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCCGGTGAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGATTTACTCCAAATGGAACAGTCATGACACA
 TGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGTACGTTAAATTTACAAATGTAACCTGTGCAAGATA
 CAGGCATGTACACATGTATGCTGAGTAATTCGTTGGGAATCACTGCTTTCAGCCACCTGAAATGTTACTGCA
 GCAACCACTACTCCTTCTCTTACTTTCAACCGTCACAGTAGAGCTATGGAACCTCTCAGGATGAGGCAGG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGTCGACTGGGAGACCAACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGCAGAGAGAAACCTTCAACCTCCAGTGACTGATATAACAGTGGGATCCCAGGAAT
 GATGAGGTATGAAGACTACCAAAATCATCATTTGGGTGTTTGTGGCCATCACACTCATGGCTGCAAGTATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAGGACTGTTGAAATTA
 TTATGTGGATGATGAGATTACGGGAGACACCCATGGAAAGCCACCTGCCATGCCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAAACACAATAAATCAATACA
 CAGTTTCAGTGCAATGAACGTTATTGATCCGAATGAACCTCTAAAGACAATGTACAAGAGACTCAAACTCTAAACAA
 TTTACAGAGTTACAAAAAACAACAATCAAAAAAAGAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGCTTTTCAAAAAAACAACAAAGAAAGAAATTTATTTATTAATAAATCTATTG
 TGATCTAAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSVSCSNQFSKVIC
 VRKNLREVPDGI STNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNPNIESIPSYAFNRIPSLRRDLGELKRLS
 YISEGAFEGLSNRLYNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCIL
 WLSWWIKDAPSNNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVDGTGMYTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGTPVVDWETTNVTTSLTPQ
 STRSTEKTFITPVDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDDEITGDTFMESHLMPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCTCGGGA
 GGGCGCCGGCGCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATC
 GGGATGTCCTCTCCTCTCTCTCTCTGCTAGTTTCTACTATGTTGGAACTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
 GTGGTGATCACTTACTCCAGTCGTATGCTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGTACACCTGTAAGGTTAAGAATTAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACTGACTTTGCAGTGTGAGTCATCTCTGGCAGAGGCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGCTCGCTCCCAATCTAGGATT
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA
 CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGAAGTAACCTGTACAGT
 ATGTACAAGCATCTGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGGTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAAAT
 AGTGCTCAGCAGCCAGCGGACACTGTCAACTGACGACAGCCACGCCAGGGGTGGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGTCTCAATTACAATGGACTTGACTCCACGCTTTTCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTCGACGGAACAGATTAGATGAGCATTTTCTTATACAATACCAACCAAGCAAA
 AGGATGTAAGCTGATTATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTAGACAGTCAAGCAGAACCACAGCCTTATTACACTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
 TTCATTTGTCATAAGGTTTGATATTAATTTCAAGGGGAGTTGAAATAGTGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGGCCAAAATAAC
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCAAAAT
 CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACACATGTCTATT
 TATCAACGCTCTTAGAAGAATTCTCTAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
 CCAACATACCATTATAGTCTCTTCTTCTGAGAAAAATGTGAAACAGAAATGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGACAGGCACCTTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCACTCCAGCTGGGTGACAGAGCGGACCTCCGTTCT

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTLTGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETGSDLTLCESSTGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSTSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

0909732.1.1001

CGCGAGGCGCGGGGACGCTGGGACGAGGACGAGAGGCCGCTACTCGACGCGCGCGGACGCGAGCGGCGACGCCA
CTTGGCGGCGCTGCTGCTGTGCTCTGTGCTCTCTGTGCGGAGTAGTGGATTCCGCGACAAATTTGAGTATCACTACT
 CTTGAAGAGTAGTATTGAAAAGGCAAAAGGGGAAATGCGTATCTGCCATGCAAAATTACCGTTAGTCGCGGAAGA
 CAGGGGAGCGCTGGACATCGAGTGCTGATATCCAGCGTGTAATCAGAAGGTGGATCAAGTGATTATTAT
 ATTTCTGGGACAAAAATTTATGATGCTACTATCCGATATCCAGTGAAGGCCGAGTACATTTTACGATATGATCTC
 AAATCTGTGATGTCATCAATAAATGTACAAATTTACAACTGTGCAGATTTGGGCATATCASTGCGAAAGTGAA
 AAAAGCTCTGGTGTGTGCAAAATAAGAAAGATTCATCTGTGTAGTCTGTGTAAGCGCTCAGGTGCGGAGATGTAC
 TTGATGGATCTGAAGAAATGGAGTGACTTTAAGTAATAAATGTGAACCAAAAAGAGGTTCACTTCATTACCA
 TATGAGTGGGCAAAATTTGTCGACTCAGCAAAAATGCCCACTGATGTTGACAGAAGATGACTTCATCTGTAT
 TCTGTAAAAAATGCCCTCTCTGTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAAGAGGTGGGCTCTGTC
 AGTCCGTGCTGGCTGTACAAGCTTGTCCCTCTCAAAATAAGCTGGAATTAATCGAGAGCAATATTAGAAGACT
 TTGCTTGCTCTAGCGCTCATTTGGCTTTATCATCTTTTCTGTCTAAAAAGGCGAGAGAAGAAAATATTGAAA
 GGAGTTGATACAGATACAGGGAAGATGTGCCACTCTCAAGAGCGCTGACTGCTCACTGCGAAGTACATCTCG
 CGATGATGATCATCTCTCTGGGTCGATGCTCTCTCCACAACTGAGGAAGATATTCTCAAGACTCAGTATAACCA
 GTACCAATGTGAAGACTTTGAACGGACTCTCAGAGTCGCACTCTCCCACTGCTAAGTTCAAGTACCCTTACAA
 GACTGATGGAATTCAGTTGTGTA**TAA**ATATGCACTATGAAGAAATCTGAAGTATTTGATTTTGACTTTATTT
 AGGCTCTAGTAAGAAGCTAAATGTTTAAAAAAGCACAGGCAAGACAGAGTATAGACAGCTGTAGAACACAC
 ATCTACTTTTATGCAATGATGATAGACATGAAGTCAGATGCTCAATCAAATATGATAGCAGCCAAATCTTTGT
 TAAAAAACCCCTATATGATAGACTGATAGTAAAGATGTTTATTATATTTCATTAAGCTACCTAACTAA
 ATTTTAACTTTTCATATGCAATTTGATATGTGGTCTTTTAGGAAAGATGTGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAATTTCTAAGTCTGTTTAAAGTTTTCCTATTAGTTAAATCAATGAAGGGAATAACCC
 TCTTTTCCCTTTTATGACACACAGAAACACGGCTTCATCGCTCAAACTATTTTATTTTTCGAACCTACA
 TGATTTGACACAAATTTCTTAAACACGACATAAATAGATTTCTCTATAAATTAATCTACATACGCTCA
 TAAAGTAAATCTCAAAGGCTGTAGAAAGCTGCTCACTCTACAGTGTCTGATATCCAACAGAGTTGTCG
 ACAATATATAATACATCAAGTCCAATATAAAAACTTGGGCACTTGACTAACTTTATAAAATTTTCAAACT
 TATCAATATCTAAGTGCTATATATTTTAAAGAAATATTCTCAATATCTCTATAAAATTAAGTTGATGG
 TTGGCCGACTTACCTTCACTACTATTATAGAAGACTTTTAACTTTTAATGTGATAGTATTTTCTACCTTT
 TTTCTCAACATGACACAAACATCAAAACAGAAAGTAGTAGGCTCAACATGTGAGGATTAATCCAGTCT
 TCCGGTCACAATGACTTCAGGAGGAGGATCCCACTGCTGCAATGGAATGGGCAATGTGGTTTATTTTCTTCC
 TGATTTGGATAACCAATGAACAGGAGGAGGATGTAGTATCTGATGGCCATCTCTCATGATCTCTGGCTT
 TTTTCTGGGCAAGGCGTGCACATTTGGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGACACAT
 TAGTTATTTCTCAAAGGAAAATTAATCATCTATCTGTCAGATTTCTCATTAAGAACAAATATCCCAACACCT
 TGATACACATCTAAGTGACACTCTTATTGTGCAGTGTAAATACATATAAAACCTCATGTGTAAATAGGCTATA
 GTATACACAGGTGACCAATATTTCTGATGATCAAAAGAAATGAATAACTCAAAACAGTACTCTCAAAAC
 CTCTCAACCAAAAGGACCAAAACATGGAACGAATGGAAGCTGTGAAGGACATCTGTTTGTATGCTCCAGTGGTT
 CCACGCTGGCTAAGCAGAGCTCACTTGAGGCGTTTAAATCAAAACACTGGAGCTGGAGCGATATATCTCT
 AGCAACTATGTCAGCAAGAGAAAATCAACTACCGCATGTCTCTACTTATAAGTGGGGAATGATGAAGAATCT
 TATGAACACAAAGAGGAACATAGACATTTGGAGTCTATTGAGGAGGGAGGGTGGGAGAGGAAGAGGACA
 GAAAGATACATTTATGATGACTGCCCTCACACTGGGTGATGAATAATATGTACAAAAATCCCTGTGACACA
 TTTTGTACTTGTGAACAAACCTCTATGTGTACCTTAAACCTAAATAAAAGTTAAAAAATAAAAAAATAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAARSLSTTPPEEMIEKAKGETAYLPCKFTLSPEDQGGPLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYPDVGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKVEVHHDIREVDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCGCTCTGATTGGTGA
 ATGGTGAAAGTGCGCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCGCTCCAGGCAGCCAGCC
 CTCAAGCATCATTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCGCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCAGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAGTCTGTTTCAAAAA
 CCACCACAATAGAAGTGTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAAACAT
 TTGTTCTCATCGTGTCAACATGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGACACAGGGCGGTTTCTGCTATTCGGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAGGCCCTTGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTCA
 AACAGTCTCCCTTCCATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAACTGAACCTCAGAGCATGAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAACATTTTCATT
 TCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAA

320/330

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMVMVLPCLGFTLLLSQVSGAQGGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

0000732.11001

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAGGAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCTGGGAGTAAAGGGTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAAATCCATATTTTACCTATGA

000072.11901

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVNHNGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

0980732-11001

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCCTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGGATGTTGGGGGCCCCGCT
CAGGCTCTGGGTCTGTGCCTTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTTTCAGAGGCAACATTTTTGGATCACACTATTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCTAATTCATTCAACACC
CCCATACACGGCGGCACACCCGGAGCGCCGAGGACGACTCGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCG
CTGG

090732 11001

324/330

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLNGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRRNEIPLIHENTPIPRRHTRSAEDDSE
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

0000732-11901

GGTAAAGGTACCCGCGAGAGACAGCCAGCAGTTCCTGTGGAGCAGCGGTGGCCGGCTAGGATG
GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACTGCGATGACAAACGACGACACAGAAG
TGCCCGCTATGACTCTAGCACCGGGCCACGCGCTCTGGAACCTCAAACGCTGAGCGCTGAG
ACCTCTTCTAGGGCCTCAACCCAGCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
GAGAAATTTCCCTTGCAAGAGAGACCAGGAGTTTCAAAAACATCTCCAACTTCATGGTGC
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCAGGGGAGCTGGAATGACC
ACAGTTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCGA
TGACAGCTCTGAAGAGGCAAAGACACTACAATGGACATATTGACATTGGCTCACACCTCCA
CAGAAGCTAAGGGCCTGTCTTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
ACCCCGTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCC
GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCTCAT
GGTCCCGGGATCTGATGTCTACTCTCTCTGCTGAAGCCTTGGTGACTGTCAAAAACCTGAG
GTTATTAATTGCAGCTACAGAAATAGAAAACAACACTTCCAGACTCTCCCTGGGCGCTCAGA
CATATGATCTCATCCCCAGGAAGGGGTGAAGCGCTCGTCCACTCCGATCACCAGCTCTGC
CTGACTCCACTGAAGCAAAACCACACATCAGTGAAGTACAGCCTCTGCGGAGACCTGTCC
ACAGCGGCACACAGAGTCACTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
CAGTTAGCAGGAATCCCTTGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTACGAGTGGGCAAAACAACCTC
CTTTGCTGGGAGCTCTGCTTCTCTCTACAGCCCTCGGAAGCCGCGCTCAAGAACTTCACCC
CTTCAGAGACACCGACCATGGACATCGAACCAAGGGGCGCTTCCCACCAGCAGGGACCT
CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCCTTAGCCAA
GATCAAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
GAGGCCGACCACAGACGTGAAGTGCAGGTGAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGAGCTCCAC
CGGGAACCTCCACGCCCACGCGCTCACTTCCAGGTCTCTTTACTGCGTGTGAGGAGAGCTA
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGTGCCCTTAGCCTG
GGCCCCCACCAGAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
CGGAGTGATGTATGGGGAGGGCTTACCTGTTCCAGAGGTGTCTTGGACTCACCTTGG
CAGATGTTCTGTGTTTTCAGTAAGAGGAGACCTGATCACCATCTGTGTGCTTCCATCTGCA
TTAAATTTCACTCAGTGTGGCCCAAAAAA

[illegible]

069877-1

[illegible][illegible]

089674

086907 11003

[illegible]

069807 1992

[illegible][illegible]

06897

[illegible]

FIGURE 327

GCGGAGCATCCGCTCGGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCCGCGG
 GCGGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCGGGGTCTCTCGAGCCCA
 GAGAGAAATCTCATCTGTGTCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAAACTGAAATTTAAATGTTCTCTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCAACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCCTGCCAGCTACGGTGCGAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCTCATTTCTACAGTTTTTACACGGGCTCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGGTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTTATAACCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTTGGTGATAGGCC
 TCGTCTCTCGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGACCCAAATGCAATGAGTTTCTGCTGACTGTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCTTCTGCTTTCTTTTTTTTTTTGGAGACAGAGCTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTCCACATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCGGCTTCCAAAGTGTCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTGGTTTTTGAAGAAGAAATGAAGT
 GGAACCAAAATAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCCTGGTTCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCCTTTAAACCTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTGAATAAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGEGSLTYTLVVICFLTLRLSASQNCCLKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMI F DTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLFSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTTSQPFTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLFLFGVLFLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCTTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGAAGAAGGCCAGGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCCTGTGGA
 ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTTCGTCTTCCAGGACCTGCTGTCTCCCTCCCCCTTCTCCAC
 CTTCAGCCTCTGGCTACAACACGCTGACGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGACGGGAGCTCCCGCCCCCCTATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTCTGCTGAGCCCTTCTGTACG
 CGCAGGCCGATGCCTTCTGACGCCACCTGCTCCTGTGGAGAAAGGAACTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTTCTGGCTCTCAGCTTGACTCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCCCTGAGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGGATTCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCCTTTCGATGTTTCA
 GCCTGACCTAGAAGCTTTGTGACCCCTGGAGCCAGCGGTGGCCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCAGTGTGCGACCCCTGCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTTCTTGAACCACCTGCATCCAGCCCTCAGGAAGCCT
 GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCAGTGACTGTGCACTTGAAGTTTGGAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTCACTTAGAGTCTGACCTTGGGCTGTGACGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACAGATCCACGTGGGGACTCCCTGAGGCTTGTAAAG
 TCCAGGCTTGGTCAGGTGAGGTGCACATTCAGGAGTAAGCCAGGACCCGGCAGAGAAGTGG
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCCTTGGCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAGAGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGCTTAACACAGAGGAGTAGGACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTCGGAGAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTTTTCTTTTTCCATTATTTATTTTAAAGACAGAATCTCGTGTCT
 CTGCCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCTCTGGGTTCAAGTGATT
 CTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGACCACCACCTGGGCTAATT
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 CTCAAATGAGCCTCTGCTTCACTCTCCCAAAATGCGGGATTACAGGATGAGCACTGTG
 TCTGGCCCTATTCTCTTTAAAGAGTGAATTAAGAGTTGTTCAAGTATGCCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAATAATGTACCCATAGTCTCAGCAGAGACTATCAT
 TATTTCTGTTTTGTGATCTCTTCCACTCTTTTCTTCTTACATAAATTGCGCGTGTCTTT
 TTTACAGAGCAATATCTTGTATATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
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 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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FPGPCCPPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTSQYTGTSPPHATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128